

Fig. 1

met ser lys asn thr
val ser ser ala arg phe arg lys val asp val asp
glu tyr asp glu asn lys phe val asp glu glu asp
gly gly asp gly gin ala gly pro asp glu gly glu
val asp ser cys leu arg gln gly asn met thr ala
ala leu gln ala ala leu lys asn pro pro ile asn
thr **arg** ser gln ala val lys asp arg ala gly ser
ile val leu lys val leu ile ser phe lys ala **gly**
asp ile glu lys ala val gln ser leu asp **arg** asn
gly val asp leu leu met lys tyr ile tyr lys gly
phe glu ser pro ser asp asn ser ser ala **val** leu
leu gln trp his glu lys ala leu ala ala gly gly
val gly ser ile val arg val leu thr ala arg lys
thr val

Fig. 2A (1/3)

ggtctgtgtg tgctgcgtg cgagtgtgtg agtgtgtgtca tattttttt tctcttttct
 ttctctctct tttttttttt tttgcaaaga aacagcagcg ccggccgcgc tccgcccagg
 cgctgcgccccc cccgggggggg ggaggcggag gaggcgggca gcggcggagg gaggggagcc
 ggggaggggggg gcgcgcgcgt gggagggagg cagcgcgcac ggtgcagccg ggcgggggg
 gaggc atg gcg ggg ccc ccg gcc cta ccc ccg ccg gag acg gcg gcg gcc
 Met Ala Gly Pro Pro Ala Leu Pro Pro Glu Thr Ala Ala Ala
 1 5 10 15

 gcc acc acg gcc ggc gcc gcc tcg tcg tcc gcc gct tcc ccg cac 338
 Ala Thr Thr Ala Ala Ala Ala Ser Ser Ser Ala Ala Ser Pro His
 20 25 30

 tac caa gag tgg att ctg gac acc atc gac tcg ctg cgc tcg cgc aag 386
 Tyr Gln Glu Trp Ile Leu Asp Thr Ile Asp Ser Leu Arg Ser Arg Lys
 35 40 45

 gcg cgg ccg gac ctg gag cgc atc tgc cgg atg gtg cgg cgg cgg cac 434
 Ala Arg Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His
 50 55 60

 ggc ccg gag ccg gag cgc acg cgc gcc gag ctc gag aaa ctg atc cag 482
 Gly Pro Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Leu Ile Gln
 65 70 75

 cag cgc gcc gtg ctc cgg gtc agc tac aag ggg agc atc tcg tac cgc 530
 Gln Arg Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg
 80 85 90 95

 aac gcg gcg cgc gtc cag ccc cgg cgc gga gcc acc ccg ccg gcc 578
 Asn Ala Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala
 100 105 110

 ccg ccg cgc gcc ccc cgc ggg ggc ccc gcc gcc gcc gcc ccg ccg 626
 Pro Pro Arg Ala Pro Arg Gly Gly Pro Ala Ala Ala Ala Pro Pro
 115 120 125

 ccc acg ccc gcc ccg ccg ccg ccc gcg ccc gtc gcc gcc gcc gcc 674
 Pro Thr Pro Ala Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala
 130 135 140

 gcc ccg gcc cgg gcg ccc cgc gcg gcc gcc gcc gct gcc gcc aca 722
 Ala Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Ala Ala Thr
 145 150 155

 gcg ccc ccc tcg ccc ggc ccc gcg cag ccg ggc ccc cgc gcg cag cgg 770
 Ala Pro Pro Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg
 160 165 170 175

 gcc gcg ccc ctg gcc gcg ccg ccc gcg ccc gcc gct ccc ccg gcg 818
 Ala Ala Pro Leu Ala Ala Pro Pro Pro Ala Pro Ala Ala Pro Pro Ala
 180 185 190

Fig. 2A (continued 2/3)

gct gct ccc ccg gcc ccg cgc cgc gcc ccc ccg ccc gcc gcc gcc Ala Ala Pro Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Ala Ala 195 200 205	866
gtc gcc gcc cggt gag tcg ccg ctg ccg ccg cca cag ccg ccg ccg Val Ala Ala Arg Glu Ser Pro Leu Pro Pro Pro Pro Gln Pro Pro Ala 210 215 220	914
ccg cca cag cag cag cag ccg ccg cca ccc ccg ccg cag cag Pro Pro Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Gln Gln 225 230 235	962
cca cag ccg ccg gag ggg ggc gct gct ccc ccg ccg ccg ccg Pro Gln Pro Pro Pro Glu Gly Ala Ala Arg Ala Gly Gly Pro Ala 240 245 250 255	1010
ccg ccc gtg agc ctg ccg gaa gtc gtg cgc tac ctc ggg ggt agc agc Arg Pro Val Ser Leu Arg Glu Val Val Arg Tyr Leu Gly Gly Ser Ser 260 265 270	1058
ggc gct ggc ggc cgc ctg acc cgc ggc cgc gtg cag ggt ctg ctg gaa Gly Ala Gly Arg Leu Thr Arg Gly Arg Val Gln Gly Leu Leu Glu 275 280 285	1106
gag gag gct gct Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu Arg Thr Arg Leu Gly Ala 290 295 300	1154
ctt gct ctg ccc cgc ggg gac agg ccc gga cgg gct ccc ccc gcc Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly Arg Ala Pro Pro Ala Ala 305 310 315	1202
agc gcc cgc gct gct Ser Ala Arg Ala Ala Arg Asn Lys Arg Ala Gly Glu Glu Arg Val Leu 320 325 330 335	1250
gaa aag gag gag gag gag gag gaa gac gac gag gac gac gac gac Glu Lys Glu Glu Glu Glu Glu Asp Asp Glu Asp Asp Asp Asp 340 345 350	1298
gac gac gtc gtg tcc gag ggc tcg gag gtg ccc gag agc gat cgt ccc Asp Asp Val Val Ser Glu Gly Ser Glu Val Pro Glu Ser Asp Arg Pro 355 360 365	1346
gct ggt gct cag cat cac cag ctg aat ggc ggc gag cgc ggc ccg cag Ala Gly Ala Gln His His Gln Leu Asn Gly Gly Glu Arg Gly Pro Gln 370 375 380	1394
acc gcc aag gag cgg gcc aag gag tgg tcg ctg tgt ggc ccc cac cct Thr Ala Lys Glu Arg Ala Lys Glu Trp Ser Leu Cys Gly Pro His Pro 385 390 395	1442
ggc cag gag gaa ggg cgg ggg ccg gcc gct ggc agt ggc acc cgc cag Gly Gln Glu Glu Gly Arg Gly Pro Ala Ala Gly Ser Gly Thr Arg Gln 400 405 410 415	1490

Fig. 2A (continued 3/3)

gtg ttc tcc atg gcg gcc ttg agt aag gag ggg gga tca gcc tct tcg Val Phe Ser Met Ala Ala Leu Ser Lys Glu Gly Gly Ser Ala Ser Ser	1538
420 425 430	
acc acc ggg cct gac tcc ccg tcc ccg gtg cct ttg ccc ccc ggg aag Thr Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro Pro Gly Lys	1586
435 440 445	
cca gcc ctc cca gga gcc gat ggg acc ccc ttt ggc tgc cct gcc ggg Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys Pro Ala Gly	1634
450 455 460	
cgc aaa gag aag ccg gca gac ccc gtg gag tgg aca gtc atg gac gtc Arg Lys Glu Lys Pro Ala Asp Pro Val Glu Trp Thr Val Met Asp Val	1682
465 470 475	
gtg gag tac ttc acc gag gcg ggc ttc cct gag caa gcc acg gct ttc Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala Thr Ala Phe	1730
480 485 490 495	
cag gag cag gag atc gac ggc aag tcc ctg ctg ctc atg cag cgc acc Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Met Gln Arg Thr	1778
500 505 510	
gat gtc ctc acc ggc ctg tcc atc cgc ctg ggg cca gcg ttg aaa atc Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala Leu Lys Ile	1826
515 520 525	
tat gag cac cat atc aag gtg ctg cag cag ggt cac ttc gag gac gat Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe Glu Asp Asp	1874
530 535 540	
gac ccg gaa ggc ttc ctg gga t gaggcacagag ccgcgcgc ccttgtcccc Asp Pro Glu Gly Phe Leu Gly	1926
545 550	
accccccaccc cgcctggacc cattcctgcc tccatgtcac ocaagggtgtc ccagaggcca ggagctggac tggcaggcg aggggtgggg acctaccctg attctggtag gggcggggc	1986
cttgctgtgc tcattgtcac ccccccaccc cgtgtgtgtc tctgcacctg ccccccagcac	2046
acccctcccg gagcctggat gtcgcctggg actctggct gtcatttttgc ccccccagatc	2106
agccccctcc tcaccctcctg tcccaggaca tttttaaaaa gaaaaaaaaaagg aaaaaaaaaa	2166
atggggagg gggctggaa ggtgcaccaa gatccctcctc ggcccaacca ggtgtttatt	2226
cctatatata tatatatatg ttttgttctg cctgtttttc gttttttgtt gcgtggcctt	2286
tcttccctcc caccaccact catggcccca gccctgtctcg ccctgtcgcc gggagcagct	2346
ggaaatggga ggagggtggg accttgggtc tgtctccac cctctctccc gttggttctg	2406
ttgtcgctcc agctggctgt attgcttttt aatattgcac cgaagggttg tttttttttt	2466
tttaaataaaa atttaaaaa aaggaaaaaa aaaaa	2526
	2561

Fig. 2B

asp cys arg ser ser ser asn asn arg Xaa pro lys
gly gly ala ala arg ala gly gly pro ala arg pro
val ser leu arg glu val val arg tyr leu gly gly
ser ser gly ala gly gly arg leu thr arg gly arg
val gln gly leu leu glu glu glu ala ala ala arg
gly arg leu glu arg thr arg leu gly ala leu ala
leu pro arg gly asp arg pro gly arg ala pro pro
ala ala ser ala arg ala ala arg asn lys arg ala
gly glu glu arg val leu glu lys glu glu glu glu
glu glu glu glu asp asp glu asp asp asp asp
val val ser glu gly ser glu val pro glu ser asp
arg pro ala gly ala gln his his gln leu asn **gly**
gly glu arg gly pro gln thr ala lys glu arg ala
lys glu trp ser leu cys gly pro his pro gly gln
glu glu gly arg gly pro ala ala gly ser gly thr
arg gln val phe ser met ala ala **leu ser lys glu**
gly gly ser ala ser ser thr thr gly pro asp ser
pro ser pro val pro leu pro pro gly lys pro ala
leu pro gly ala asp gly thr pro phe gly cys pro
ala gly arg lys glu lys pro ala asp pro val glu
trp thr val met asp val val glu tyr phe thr glu
ala gly phe pro glu gln ala thr ala phe gln glu
gln glu ile asp gly lys ser leu leu leu met gln
arg thr asp val leu thr gly leu ser ile arg leu
gly pro ala leu lys ile tyr glu his his ile lys
val leu gln gln gly his phe glu asp asp asp pro
glu gly phe leu gly

Fig. 3

ala ser ala arg ala ala arg asn lys arg ala
gly glu glu arg val leu glu lys glu glu glu
glu glu glu glu asp asp glu asp asp asp asp
val val ser glu gly ser glu val pro glu ser asp
arg pro ala gly ala gln his his gln leu asn gly
gly glu arg gly pro gln **thr** ala lys glu arg ala
lys glu trp **ser** leu cys gly pro his **pro** gly gln
glu glu gly arg gly pro ala **ala** gly ser gly thr
arg gln val phe ser met ala ala **leu ser** lys glu
gly gly **ser** ala ser **ser thr** thr gly pro asp ser
pro ser pro val pro leu pro pro gly lys pro ala
leu pro gly ala asp gly thr pro phe gly cys pro
ala gly arg lys glu lys pro **ala** asp pro val glu
trp thr val met asp val val glu tyr phe thr glu
ala gly phe pro glu gln ala thr ala phe gln glu
gln glu ile asp gly lys ser leu leu leu met gln
arg thr asp val leu thr gly leu **ser** ile arg leu
gly pro ala leu lys ile tyr glu his his ile lys
val leu gln gln gly his phe glu asp asp asp pro
glu gly phe leu gly

Fig. 4

thr arg leu gly ala leu ala
leu pro arg gly asp arg pro gly arg ala pro pro
ala ala ser ala arg ala ala arg asn lys arg ala
gly glu glu arg val leu glu lys glu glu glu
glu glu glu glu asp **asp** glu **asp** **asp** asp asp **asp**
val val ser glu gly ser glu val pro glu ser asp
arg pro ala gly ala gln his his gln leu asn **gly**
gly glu arg gly pro gln **thr** ala lys glu arg **ala**
lys glu trp **ser** **leu** cys gly pro his **pro** gly gln
glu glu gly arg gly pro ala **ala** gly ser gly thr
arg gln val phe ser met ala ala **leu** **ser** lys glu
gly gly **ser** ala ser **ser** **thr** thr gly pro asp ser
pro ser pro val pro leu pro pro gly lys pro ala
leu pro gly ala asp gly thr pro phe gly cys pro
ala gly arg lys glu lys pro **ala** asp pro val glu
trp thr val met asp val val glu tyr phe thr glu
ala gly phe pro glu gln ala thr ala phe gln glu
gln glu ile asp gly lys ser leu leu leu met gln
arg thr asp val leu thr gly leu ser ile arg leu
gly pro ala leu lys ile tyr glu his his ile lys
val leu gln gln gly his phe glu asp asp asp pro
glu gly phe leu gly

Fig. 5

met lys asn gln
asp lys lys asn gly ala ala lys gln pro asn pro
lys ser ser pro gly gln pro glu ala gly **ala** glu
gly ala gln **gly** arg pro **gly arg pro** ala pro ala
arg glu ala glu gly **ala** ser ser gln ala pro **gly**
arg pro glu gly ala gln ala **lys** thr ala gln **pro**
gly ala leu **cys** asp val ser glu glu leu ser arg
gln leu glu asp ile leu ser thr tyr cys val asp
asn asn gln gly **ala** pro gly glu asp gly **val** gln
gly glu pro **pro** glu pro glu asp ala glu lys ser
arg **ala** tyr val ala arg asn gly glu pro glu pro
gly thr pro val val **asn** gly glu lys glu **thr** ser
lys **ala** glu pro **gly** thr glu glu ile arg **thr** ser
asp glu val gly asp arg asp his arg arg pro gln
glu lys lys ala lys gly leu gly lys glu ile
thr leu leu met gln thr leu asn thr leu ser thr
pro glu glu lys leu ala ala leu cys lys tyr
ala glu leu leu glu glu his arg asn ser gln lys
gln met lys leu leu gln lys lys gln ser gln leu
val gln glu lys asp his leu arg gly glu his ser
lys ala **ile** leu ala arg ser lys leu glu ser leu
cys arg glu leu gln arg his asn arg ser leu lys
glu glu gly val gln arg ala arg glu glu glu
lys arg lys glu val thr ser his phe gln **met** thr
leu asn asp ile gln leu gln met glu gln his asn
glu arg asn ser lys leu arg gln glu asn met glu

Fig. 5 (continued)

leu ala glu arg leu lys lys leu ile glu gln tyr
glu leu arg glu glu his ile asp lys val phe lys
his lys asp leu gln gln leu val asp ala lys
leu gln gln ala gln glu met leu lys glu ala glu
glu arg his gln arg glu lys asp phe leu leu lys
glu ala val glu ser gln arg met cys glu leu met
lys gln gln glu thr his leu lys gln gln leu ala
leu tyr thr glu lys phe glu glu phe gln asn thr
leu ser lys ser ser glu val phe thr thr phe lys
gln glu met glu lys met thr lys lys ile lys lys
leu glu lys glu thr thr met tyr arg ser arg trp
glu ser ser asn lys ala leu leu glu met ala glu
glu lys thr leu arg asp lys glu leu glu gly leu
gln val lys ile gln arg leu glu lys leu cys arg
ala leu gln thr glu arg asn asp leu asn lys arg
val gln asp leu ser ala gly gly gln gly pro val
ser asp ser gly pro glu arg arg pro glu pro ala
thr thr ser lys glu gln gly val glu gly pro gly
ala gln val pro asn ser pro arg ala thr asp ala
ser cys cys ala gly ala pro ser thr glu ala ser
gly gln thr gly pro gln glu pro thr thr ala thr
ala

Fig. 6

met ser lys asn thr val ser ser ala
arg phe arg lys val asp val asp glu tyr asp glu
asn lys phe val asp glu glu asp gly gly asp gly
gln ala gly pro asp glu gly glu val asp ser cys
leu arg gln gly asn met thr ala ala leu gln ala
ala leu lys asn pro pro ile asn thr **lys** ser gln
ala val lys asp arg ala gly ser ile val leu lys
val leu ile ser phe lys ala **asn** asp ile glu lys
ala val gln ser leu asp **lys** asn gly val asp leu
leu met lys tyr ile tyr lys gly phe glu ser pro
ser asp asn ser ser ala **met** leu leu gln trp his
glu lys ala leu ala ala gly gly val gly ser ile
val arg val leu thr ala arg lys thr val

Fig. 7A (1/3)

atg gcg ggg ccc ccg gcc cta ccc ccg ccg gag acg gcg gcg gcc gcc Met Ala Gly Pro Pro Ala Leu Pro Pro Pro Glu Thr Ala Ala Ala Ala 1 5 10 15	48
acc acg gcg gcc gcc tcg tcg tcc gcc gct tcc ccg cac tac caa Thr Thr Ala Ala Ala Ser Ser Ala Ala Ser Pro His Tyr Gln 20 25 30	96
gag tgg atc ctg gac acc atc gac tcg ctg cgc tcg cgc aag gcg cgg Glu Trp Ile Leu Asp Thr Ile Asp Ser Leu Arg Ser Arg Lys Ala Arg 35 40 45	144
ccg gac ctg gag cgc atc tgc cgg atg gtg cgg cgg cgg cac ggc ccg Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His Gly Pro 50 55 60	192
gag ccg gag cgc acg cgc gcc gag ctc gag aaa ctg atc cag cag cgc Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Ile Gln Gln Arg 65 70 75 80	240
gcc gtg ctc cgg gtc agc tac aag ggg agc atc tcg tac cgc aac gcg Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg Asn Ala 85 90 95	288
gcg cgc gtc cag ccg ccc cgg cgc gga gcc acc ccg ccg gcc ccg ccg Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala Pro Pro 100 105 110	336
cgc gcc ccc cgc ggg gcc ccc gcc gcc gcc gcc gcc gcg ccg ccg Arg Ala Pro Arg Gly Ala Pro Ala Ala Ala Ala Ala Ala Pro Pro 115 120 125	384
ccc acg ccc gcc ccg cca ccg ccc gcg ccc gtc gcc gcc gcc gcc Pro Thr Pro Ala Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala 130 135 140	432
ccg gcc cgg gcg ccc cgc gcg gcc gcc gcc gcc aca gcg ccc ccc Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Thr Ala Pro Pro 145 150 155 160	480
tcg cct ggc ccc gcg cag ccg ggc ccc cgc gcg cag ccg gcc gcg ccc Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg Ala Ala Pro 165 170 175	528
ctg gcc gcg ccg ccc gcg cca gcc gct ccc ccg gcg gtg gcg ccc Leu Ala Ala Pro Pro Ala Pro Ala Pro Pro Ala Val Ala Pro 180 185 190	576
ccg gcc ggc ccg cgc cgc gcc ccc ccg ccc gcc gtc gcc gcc ccg gag Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Val Ala Ala Arg Glu 195 200 205	624
ccg ccg ctg ccg ccg cca cag ccg ccg gcg cca cag cag cag Pro Pro Leu Pro Pro Pro Gln Pro Pro Ala Pro Pro Gln Gln Gln 210 215 220	672

Fig. 7A (continued; 2/3)

cag ccg ccg ccg cag cca cag ccg ccg ccg gag ggg ggc gcg	720
Gln Pro Pro Pro Pro Gln Pro Pro Pro Glu Gly Gly Ala Val	
225 230 235 240	
 cgg gcc ggc ggc gcg ccg gtg agc ctg ccg gaa gtc gtg cgc	768
Arg Ala Gly Gly Ala Ala Arg Pro Val Ser Leu Arg Glu Val Val Arg	
245 250 255	
 tac ctc ggg ggc agc ggc ggc ggc ggt cgc cta acc cgc ggc cgc	816
Tyr Leu Gly Gly Ser Gly Gly Ala Gly Arg Leu Thr Arg Gly Arg	
260 265 270	
 gtg cag ggg ctg ctg gag gag gac gcg gct cga ggc cgt ctg gag	864
Val Gln Gly Leu Leu Glu Glu Ala Ala Arg Gly Arg Leu Glu	
275 280 285	
 cgc acc cgt ctc gga gcg ctt gcg ctg ccc cgc ggg gac agg ccc gga	912
Arg Thr Arg Leu Gly Ala Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly	
290 295 300	
 cgg gcg ccg ccg gcc agc gcc cgc ccg tct cgc agc aag aga ggt	960
Arg Ala Pro Pro Ala Ala Ser Ala Arg Pro Ser Arg Ser Lys Arg Gly	
305 310 315 320	
 gga gaa gag cga gta ctt gag aaa gaa gag gaa gaa gat gat gat gaa	1008
Gly Glu Glu Arg Val Leu Glu Lys Glu Glu Glu Asp Asp Asp Glu	
325 330 335	
 gat gaa gat gaa gaa gat gat gtg tca gag ggc tct gaa gtg ccc gag	1056
Asp Glu Asp Glu Asp Asp Val Ser Glu Gly Ser Glu Val Pro Glu	
340 345 350	
 agt gac cgt cct gca ggt gcc cag cac cac cag ctt aac ggc gag cgg	1104
Ser Asp Arg Pro Ala Gly Ala Gln His His Gin Leu Asn Gly Glu Arg	
355 360 365	
 gga cct cag agt gcc aag gag agg gtc aag gag tgg acc ccc tgc gga	1152
Gly Pro Gln Ser Ala Lys Glu Arg Val Lys Glu Trp Thr Pro Cys Gly	
370 375 380	
 ccg cac cag ggc cag gat gaa ggg cgg ggg cca gcc ccg ggc agc ggc	1200
Pro His Gln Gly Gln Asp Glu Gly Arg Gly Pro Ala Pro Gly Ser Gly	
385 390 395 400	
 acc cgc cag gtg ttc tcc atg gca gcc atg aac aag gaa ggg gga aca	1248
Thr Arg Gln Val Phe Ser Met Ala Ala Met Asn Lys Glu Gly Gly Thr	
405 410 415	
 gct tct gtt gcc acc ggg cca gac tcc ccg tcc ccc gtg cct ttg ccc	1296
Ala Ser Val Ala Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro	
420 425 430	
 cca ggc aaa cca gcc cta cct ggg gcc gac ggg acc ccc ttt ggc tgt	1344
Pro Gly Lys Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys	
435 440 445	

Fig. 7A (continued; 3/3)

ccg ccc ggg cgc aaa gag aag cca tct gat ccc gtc gag tgg acc gtg	1392
Pro Pro Gly Arg Lys Glu Lys Pro Ser Asp Pro Val Glu Trp Thr Val	
450 455 460	
atg gat gtc gtc gaa tat ttt act gag gct gga ttc ccg gag caq gcg	1440
Met Asp Val Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala	
465 470 475 480	
aca gct ttc caa gag caq gaa att gat ggc aaa tct ttg ctg ctc atg	1488
Thr Ala Phe Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Met	
485 490 , 495	
cag cgc aca gat gtg ctc acc ggc ctg tcc atc cgc ctc ggg cca gcc	1536
Gln Arg Thr Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala	
500 505 510	
ctg aaa atc tac gag cac cac atc aag gtg ctt cag caa ggc cac ttt	1584
Leu Lys Ile Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe	
515 520 525	
gag gat gat gac ccc gat ggc ttc tta ggc	1614
Glu Asp Asp Asp Pro Asp Gly Phe Leu Gly	
530 535	

Fig. 7B

glu glu arg val leu glu lys glu glu glu **asp**
asp **asp** glu asp glu **asp** glu glu asp asp val ser
glu gly ser glu val pro glu ser asp arg pro ala
gly ala gln his his gln leu asn gly glu arg gly
pro gln **ser** ala lys glu arg **val** lys glu trp **thr**
pro cys gly pro his **gln** gly gln **asp** glu gly arg
gly pro ala **pro** gly ser gly thr arg gln val phe
ser met ala ala **met** **asn** lys glu gly gly **thr** ala
ser **val** **ala** thr gly pro asp ser pro ser pro val
pro leu pro pro gly lys pro ala leu pro gly ala
asp gly thr pro phe gly cys pro **pro** gly arg lys
glu lys pro **ser** asp pro val glu trp thr val met
asp val val glu tyr phe thr glu ala gly phe pro
glu gln ala thr ala phe gln glu gln glu ile asp
gly lys ser leu leu leu met gln arg thr asp val
leu thr gly leu ser ile arg leu gly pro ala leu
lys ile tyr glu his his ile lys val leu gln gln
gly his phe glu asp asp asp pro **asp** gly phe leu
gly

Fig. 8A (1/3)

atg aag aac caa gac aaa aag aac ggg gct gcc aaa caa tcc aat cca Met Lys Asn Gln Asp Lys Lys Asn Gly Ala Ala Lys Gln Ser Asn Pro 1 5 10 15	48
aaa agc agc cca gga caa ccg gaa gca gga ccc gag gga gcc cag gag Lys Ser Ser Pro Gly Gln Pro Glu Ala Gly Pro Glu Gly Ala Gln Glu 20 25 30	96
cgg ccc agc cag gcg gct cct gca gta gaa gca gaa ggt ccc ggc agc Arg Pro Ser Gln Ala Ala Pro Ala Val Glu Ala Glu Gly Pro Gly Ser 35 40 45	144
agc cag gct cct cgg aag ccg gag ggt gct caa gcc aga acg gct cag Ser Gln Ala Pro Arg Lys Pro Glu Gly Ala Gln Ala Arg Thr Ala Gln 50 55 60	192
tct ggg gcc ctt cgt gat gtc tct gag gag ctg agc cgc caa ctg gaa Ser Gly Ala Leu Arg Asp Val Ser Glu Glu Leu Ser Arg Gln Leu Glu 65 70 75 80	240
gac ata ctg agc aca tac tgt gtg gac aat aac cag ggg ggc ccc ggc Asp Ile Leu Ser Thr Tyr Cys Val Asp Asn Asn Gln Gly Gly Pro Gly 85 90 95	288
gag gat ggg gca cag ggt gag ccg gct gaa ccc gaa gat gca gag aag Glu Asp Gly Ala Gln Gly Glu Pro Ala Glu Pro Glu Asp Ala Glu Lys 100 105 110	336
tcc cgg acc tat gtg gca agg aat ggg gag cct gaa cca act cca gta Ser Arg Thr Tyr Val Ala Arg Asn Gly Glu Pro Glu Pro Thr Pro Val 115 120 125	384
gtc aat gga gag aag gaa ccc tcc aag ggg gat cca aac aca gaa gag Val Asn Gly Glu Lys Glu Pro Ser Lys Gly Asp Pro Asn Thr Glu Glu 130 135 140	432
atc cgg cag agt gac gag gtc gga gac cga gac cat cga agg cca cag Ile Arg Gln Ser Asp Glu Val Gly Asp Arg Asp His Arg Arg Pro Gln 145 150 155 160	480
gag aag aaa aaa gcc aag ggt ttg ggt aag gag atc acg ttg ctg atg Glu Lys Lys Lys Ala Lys Gly Leu Gly Lys Glu Ile Thr Leu Leu Met 165 170 175	528
cag aca ttg aat act ctg agt acc cca gag gag aag ctg gct gct ctg Gln Thr Leu Asn Thr Leu Ser Thr Pro Glu Glu Lys Leu Ala Ala Leu 180 185 190	576
tgc aag aag tat gct gaa ctg ctg gag gag cac cgg aat tca cag aag Cys Lys Lys Tyr Ala Glu Leu Glu Glu His Arg Asn Ser Gln Lys 195 200 205	624

Fig. 8A (continued; 2/3)

cag atg aag ctc cta cag aaa aag cag agc cag ctg gtg caa gag aag Gln Met Lys Leu Leu Gln Lys Lys Gln Ser Gln Leu Val Gln Glu Lys 210 215 220	672
gac cac ctg cgc ggt gag cac agc aag gcc gtc ctg gcc cgc agc aag Asp His Leu Arg Gly Glu His Ser Lys Ala Val Leu Ala Arg Ser Lys 225 230 235 240	720
ctt gag agc cta tgc cgt gag ctg cag cgg cac aac cgc tcc ctc aag Leu Glu Ser Leu Cys Arg Glu Leu Gln Arg His Asn Arg Ser Leu Lys 245 250 255	768
gaa gaa ggt gtg cag cgg gcc cgg gag gag gag aag cgc aag gag Glu Glu Gly Val Gln Arg Ala Arg Glu Glu Glu Lys Arg Lys Glu 260 265 270	816
gtg acc tcg cac ttc cag gtg aca ctg aat gac att cag ctg cag atg Val Thr Ser His Phe Gln Val Thr Leu Asn Asp Ile Gln Leu Gln Met 275 280 285	864
gaa cag cac aat gag cgc aac tcc aag ctg cgc caa gag aac atg gag Glu Gln His Asn Glu Arg Asn Ser Lys Leu Arg Gln Glu Asn Met Glu 290 295 300	912
ctg gct gag agg ctc aag aag ctg att gag cag tat gag ctg cgc gag Leu Ala Glu Arg Leu Lys Leu Ile Glu Gln Tyr Glu Leu Arg Glu 305 310 315 320	960
gag cat atc gac aaa gtc ttc aaa cac aag gac cta caa cag cag ctg Glu His Ile Asp Lys Val Phe Lys His Lys Asp Leu Gln Gln Leu 325 330 335	1008
gtg gat gcc aag ctc cag cag gcc cag gag atg cta aag gag gca gaa Val Asp Ala Lys Leu Gln Gln Ala Glu Met Leu Lys Glu Ala Glu 340 345 350	1056
gag cgg cac cag cgg gag aag gat ttt ctc ctg aaa gag gca gta gag Glu Arg His Gln Arg Glu Lys Asp Phe Leu Leu Lys Glu Ala Val Glu 355 360 365	1104
tcc cag agg atg tgt gag ctg atg aag cag caa gag acc cac ctg aag Ser Gln Arg Met Cys Glu Leu Met Lys Gln Gln Glu Thr His Leu Lys 370 375 380	1152
caa cag ctt gcc cta tac aca gag aag ttt gag gag ttc cag aac aca Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln Asn Thr 385 390 395 400	1200
ctt tcc aaa agc agc gag gta ttc acc aca ttc aag cag gag atg gaa Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu Met Glu 405 410 415	1248

Fig. 8A (continued; 3/3)

aag atg act aag aag atc aag aag ctg gag aaa gaa acc acc atg tac Lys Met Thr Lys Lys Ile Lys Lys Leu Glu Lys Glu Thr Thr Met Tyr 420 425 430	1296
cgg tcc cgg tgg gag agc agc aac aag gcc ctg ctt gag atg gct gag Arg Ser Arg Trp Glu Ser Ser Asn Lys Ala Leu Leu Glu Met Ala Glu 435 440 445	1344
gag aaa aca gtc cgg gat aaa gaa ctg gag ggc ctg cag gta aaa atc Glu Lys Thr Val Arg Asp Lys Glu Leu Glu Gly Leu Gln Val Lys Ile 450 455 460	1392
caa cgg ctg gag aag ctg tgc cgg gca ctg cag aca gag cgc aat gac Gln Arg Leu Glu Lys Leu Cys Arg Ala Leu Gln Thr Glu Arg Asn Asp 465 470 475 480	1440
ctg aac aag agg gta cag gac ctg agt gct ggt ggc cag ggc tcc ctc Leu Asn Lys Arg Val Gln Asp Leu Ser Ala Gly Gly Gln Gly Ser Leu 485 490 495	1488
act gac agt ggc cct gag agg agg cca gag ggg cct ggg gct caa gca Thr Asp Ser Gly Pro Glu Arg Arg Pro Glu Gly Pro Gly Ala Gln Ala 500 505 510	1536
ccc agc tcc ccc agg gtc aca gaa gcg cct tgc tac cca gga gca ccg Pro Ser Ser Pro Arg Val Thr Glu Ala Pro Cys Tyr Pro Gly Ala Pro 515 520 525	1584
agc aca gaa gca tca ggc cag act ggg cct caa gag ccc acc tcc gcc Ser Thr Glu Ala Ser Gly Gln Thr Gly Pro Gln Glu Pro Thr Ser Ala 530 535 540	1632
agg gcc Arg Ala 545	1638

Fig. 8 B

lys ser ser pro gly gln pro glu ala gly pro glu gly ala
gln glu arg pro ser gln ala ala pro ala val glu ala glu gly
pro gly ser ser gln ala pro arg lys pro glu gly ala gln ala
arg thr ala gln ser gly ala leu arg asp val ser glu glu leu
ser arg gln leu glu asp ile leu ser thr tyr cys val asp asn
asn gln gly gly pro gly glu asp gly ala gln gly glu pro ala
glu pro glu asp ala glu lys ser arg thr tyr val ala arg asn
gly glu pro glu pro thr pro val val tyr gly glu lys glu pro
ser lys gly asp pro asn thr glu glu ile arg gln ser asp glu
val gly asp arg asp his arg arg pro gln glu lys lys ala
lys gly leu gly lys glu ile thr leu leu met gln thr leu asn
thr leu ser thr pro glu glu lys leu ala ala leu cys lys lys
tyr ala glu leu leu glu glu his arg asn ser gln lys gln met
lys leu leu gln lys gln ser gln leu val gln glu lys asp
his leu arg gly glu his ser lys ala val leu ala arg ser lys
leu glu ser leu cys arg glu leu gln arg his asn arg ser leu
lys glu glu gly val gln arg ala arg glu glu glu lys arg
lys glu val thr ser his phe gln val thr leu asn asp ile gln
leu gln met glu gln his asn glu arg asn ser lys leu arg gln
glu asn met glu leu ala glu arg leu lys lys leu ile glu gln
tyr glu leu arg glu glu his ile asp lys val phe lys his lys
asp leu gln gln leu val asp ala lys leu gln gln ala gln
glu met leu lys glu ala glu glu arg his gln arg glu lys asp
phe leu leu lys glu ala val glu ser gln arg met cys glu leu
met lys gln gln glu thr his leu lys gln gln leu ala leu tyr
thr glu lys phe glu glu phe gln asn thr leu ser lys ser ser

Fig. 8 B(continued)

glu val phe thr thr phe lys gln glu met glu lys met thr lys
lys ile lys lys leu glu lys glu thr thr met tyr arg ser arg
trp glu ser ser asn lys ala leu leu glu met ala glu glu lys
thr **val** arg asp lys glu leu glu gly leu gln val lys ile gln
arg leu glu lys leu cys arg ala leu gln thr glu arg asn asp
leu asn lys arg val gln asp leu ser ala gly gly gln gly **ser**
leu **thr** asp ser gly pro glu arg arg pro glu gly pro gly ala
gln ala pro **ser** ser pro arg val thr glu ala **pro** cys **tyr** pro
gly ala pro ser thr glu ala ser gly gln thr gly pro gln glu
pro thr **ser** ala **arg** ala ***

Fig. 9

val asp val asp

glu tyr asp glu asn lys phe val asp glu glu asp

gly gly asp gly

Fig. 10

1 AAG CCT CGC AGC GGT CGG GGC GGC GCC GCG GAG GCT
37 CGA GGG CGG CGG GCG GCG GCG ATG TCG AAG AAC ACG
met ser lys asn thr

73 GTG TCG TCG GCG CGG TTC CGG AAG GTG GAC GTG GAT
val ser ser ala arg phe arg lys val asp val asp

109 GAG TAC GAC GAG AAC AAG TTC GTG GAC GAG GAA GAC
glu tyr asp glu asn lys phe val asp glu glu asp

145 GGC GGC GAC GGC CAG GCG GGG CCG GAC GAG GGC GAG
gly gly asp gly gln ala gly pro asp glu gly glu

181 GTG GAC TCG TGC CTG CGG CAA GGG AAC ATG ACA GCC
val asp ser cys leu arg gln gly asn met thr ala

217 GCC CTG CAG GCG GCG CTG AAG AAC CCT CCC ATC AAC
ala leu gln ala ala leu lys asn pro pro ile asn

253 ACC AGG AGC CAG GCG GTG AAG GAC CGG GCA GGC AGC
thr **arg** ser gln ala val lys asp arg ala gly ser

289 ATC GTG CTG AAG GTG CTC ATC TCC TTC AAG GCC GGC
ile val leu lys val leu ile ser phe lys ala **gly**

325 GAC ATA GAA AAG GCC GTG CAG TCC CTG GAC AGG AAC
asp ile glu lys ala val gln ser leu asp **arg** asn

361 GGC GTG GAC CTG CTC ATG AAG TAC ATC TAC AAG GGC
gly val asp leu leu met lys tyr ile tyr lys gly

397 TTC GAG AGC CCC TCC GAC AAC AGC AGC GCC GTG CTC
phe glu ser pro ser asp asn ser ser ala **val** leu

433 CTG CAG TGG CAC GAG AAG GCG CTG GCT GCA GGA GGA
leu gln trp his glu lys ala leu ala ala gly gly

469 GTG GGC TCC ATC GTC CGT GTC CTG ACT GCA AGG AAA
val gly ser ile val arg val leu thr ala arg lys

505 ACC GTG TAG CCT GGC AGG AAC GGG TGC CTG CCG GGG
thr val

Fig. 10 (continued)

541 AGC GGG AGC TGC CGG TAC AAA GAC CAA AAC GCC CAG
577 ATG CCG CCG CTG CCC TGT GGG CGG CGT CTG TTC CCA
613 GCT TCG CTT TTT CCC TTT CCC GTG TCT GTC AGG ATT
649 ACA TAA GGT TTC CCT TCG TGA GAA TCG GAG TGG CGC
685 AGA GGG TCC TGT TCA TAC GCG CCG TGC GTC CGG CTG
721 TGT AAG ACC CCT GCC TTC AGT GTC CTT GAG CAA CGG
757 TAG CGT GTC GCC GGC TGG GTT TGG TTT TGT CGT GGA
793 GGG ATC TGG TCA GAA TTT GAG GCC AGT TTC CTA ACT
829 CAT TGC TGG TCA GGA AAT GAT CTT CAT TTA AAA AAA
865 AAA AAA AGA CTG GCA GCT ATT ATG CAA AAC TGG ACC
901 CTC TTC CCT TAT TTA AGC AGA GTG AGT TTC TGG AAC
937 CAG TGG TGC CCC CCC CCC CGC CCC GGC CGC CGT CCT
973 GCT CAA GGG AAG CCT CCC TGC AGA GCA GCA GAG CCC
1009 CTG GGC AGG AGC GCC GCG TCC CGC TCC CAG GAG ACA
1045 GCA TGC GCG GTC ACG CGG CAC TTC CTG TGC CTC CCA
1081 GCC CCA GTG CCC CGG AGT TCT TCA GGG CGA CAG GGA
1117 CCT CAG AAG ACT GGA TCC GAT CCA GAC AGA CGC CCA
1153 TTC TTG GTT CAG CTC AGT GTT TTC AAA AGG AAC GTG
1189 CTA CCG TGG GTA GAG CAC ACT GGT TCT CAG AAC ACG
1225 GCC GGC GCT TGA CGG TTG TCA CAG CTC CAG AAC AAA
1261 TCC TGG GAG ACA GGC GAG CGC GAG TCG CCG GGC AGG
1297 AAT TCC ACA CAC TCG TGC TGT TTT TGA TAC CTG CTT
1333 TTT GTT TTG TTT TGT AAA AAT GAT GCA CTT GAG AAA
1369 ATA AAA CGT CAG TGT TGA CAA AAA AAA AAA AAA AAA

Fig. 11

1 GAC TGC CGC AGC AGC AAC AAC CGC TAG CCG AAG
asp cys arg ser ser ser asn asn arg Xaa pro lys

37 GGT GGC GCG GCG CGG GCC GGC CCG GCG CGG CCC
gly gly ala ala arg ala gly gly pro ala arg pro

73 GTG AGC CTG CGG GAA GTC GTG CGC TAC CTC GGG GGT
val ser leu arg glu val val arg tyr leu gly gly

109 AGC AGC GGC GCT GGC GGC CGC CTG ACC CGC GGC CGC
ser ser gly ala gly gly arg leu thr arg gly arg

145 GTG CAG GGT CTG CTG GAA GAG GAG GCG GCG GCG CGG
val gln gly leu leu glu glu glu ala ala ala arg

181 GGC CGC CTG GAG CGC ACC CGT CTC GGA GCG CTT GCG
gly arg leu glu arg thr arg leu gly ala leu ala

217 CTG CCC CGC GGG GAC AGG CCC GGA CGG GCG CCA CCG
leu pro arg gly asp arg pro gly arg ala pro pro

253 GCC GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT
ala ala ser ala arg ala ala arg asn lys arg ala

289 GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG GAG
gly glu glu arg val leu glu lys glu glu glu glu

325 GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC GAC
glu glu glu glu asp asp glu asp asp asp asp asp

361 GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT
val val ser glu gly ser glu val pro glu ser asp

397 CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC
arg pro ala gly ala gln his his gln leu asn **gly**

433 GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC
gly glu arg gly pro gln **thr** ala lys glu arg **ala**

469 AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG
lys glu trp **ser** leu cys gly pro his **pro** gly gln

Fig. 11 (continued)

505 GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC
glu glu gly arg gly pro ala **ala** gly ser gly thr

541 CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG
arg gln val phe ser met ala ala **leu** **ser** lys glu

577 GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC
gly gly **ser** ala ser **ser** **thr** thr gly pro asp ser

613 CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC
pro ser pro val pro leu pro pro gly lys pro ala

649 CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT
leu pro gly ala asp gly thr pro phe gly cys pro

685 GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG
ala gly arg lys glu lys pro **ala** asp pro val glu

721 TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG
trp thr val met asp val val glu tyr phe thr glu

757 GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG
ala gly phe pro glu gln ala thr ala phe gln glu

793 CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG
gln glu ile asp gly lys ser leu leu leu met gln

829 CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG
arg thr asp val leu thr gly leu ser ile arg leu

865 GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG
gly pro ala leu lys ile tyr glu his his ile lys

901 GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG
val leu gln gln gly his phe glu asp asp asp pro

937 GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC
glu gly phe leu gly

973 CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC

1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG

1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC

1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT

Fig. 11 (continued)

1117 TGC TAC CCC CCC ACC CCG TGT GTG TCT CTG CAC CTG
1153 CCC CCA GCA CAC CCC TCC CGG AGC CTG GAT GTC GCC
1189 TGG GAC TCT GGC CTG CTC ATT TTG CCC CCA GAT CAG
1225 CCC CCT CCC TCC CTC CTG TCC CAG GAC ATT TTT TAA
1261 AAG AAA AAA AGG AAA AAA AAA AAT TGG GGA GGG GGC
1297 TGG GAA GGT GCC CCA AGA TCC TCC TCG GCC CAA CCA
1333 GGT GTT TAT TCC TAT ATA TAT ATA TAT ATG TTT TGT
1369 TCT GCC TGT TTT TCG TTT TTT GGT GCG TGG CCT TTC
1405 TTC CCT CCC ACC ACC ACT CAT GGC CCC AGC CCT GCT
1441 CGC CCT GTC GGC GGG AGC AGC TGG GAA TGG GAG GAG
1477 GGT GGG ACC TTG GGT CTG TCT CCC ACC CTC TCT CCC
1513 GTT GGT TCT GTT GTC GCT CCA GCT GGC TGT ATT GCT
1549 TTT TAA TAT TGC ACC GAA GGG TTG TTT TTT TTT TTT
1585 TAA ATA AAA TTT TAA AAA AAG GAA AAA AAA AAA

Fig. 12

256 GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT
ala ser ala arg ala ala arg asn lys arg ala

289 GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG
gly glu glu arg val leu glu lys glu glu glu

325 GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC
glu glu glu glu asp asp asp asp asp asp asp asp

361 GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT
val val ser glu gly ser glu val pro glu ser asp

397 CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC
arg pro ala gly ala gln his his gln leu asn gly

433 GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC
gly glu arg gly pro gln thr ala lys glu arg ala

469 AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG
lys glu trp ser leu cys gly pro his pro gly gln

505 GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC
glu glu gly arg gly pro ala ala gly ser gly thr

541 CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG
arg gln val phe ser met ala ala leu ser lys glu

577 GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC
gly gly ser ala ser ser thr thr gly pro asp ser

613 CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC
pro ser pro val pro leu pro pro gly lys pro ala

649 CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT
leu pro gly ala asp gly thr pro phe gly cys pro

685 GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG
ala gly arg lys glu lys pro ala asp pro val glu

721 TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG
trp thr val met asp val val glu tyr phe thr glu

Fig. 12 (continued)

757 GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG
ala gly phe pro glu gln ala thr ala phe gln glu

793 CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG
gln glu ile asp gly lys ser leu leu leu met gln

829 CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG
arg thr asp val leu thr gly leu ser ile arg leu

865 GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG
gly pro ala leu lys ile tyr glu his his ile lys

901 GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG
val leu gln gln gly his phe glu asp asp asp pro

937 GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC
glu gly phe leu gly

973 CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC
1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG
1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC
1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT
1117 TGC TAC CCC CCC ACC CCG TGT GTG TCT CTG CAC CTG
1153 CCC CCA GCA CAC CCC TCC CGG AGC CTG GAT GTC GCC
1189 TGG GAC TCT GGC CTG CTC ATT TTG CCC CCA GAT CAG
1225 CCC CCT CCC TCC CTC CTG TCC CAG GAC ATT TTT TAA
1261 AAG AAA AAA AGG AAA AAA AAA AAT TGG GGA GGG GGC
1297 TGG GAA GGT GCC CCA AGA TCC TCC TCG GCC CAA CCA
1333 GGT GTT TAT TCC TAT ATA TAT ATA TAT ATG TTT TGT
1369 TCT GCC TGT TTT TCG TTT TTT GGT GCG TGG CCT TTC
1405 TTC CCT CCC ACC ACC ACT CAT GGC CCC AGC CCT GCT
1441 CGC CCT GTC GGC GGG AGC AGC TGG GAA TGG GAG GAG
1477 GGT GGG ACC TTG GGT CTG TCT CCC ACC CTC TCT CCC
1513 GTT GGT TCT GTT GTC GCT CCA GCT GGC TGT ATT GCT
1549 TTT TAA TAT TGC ACC GAA GGG TTG TTT TTT TTT TTT
1585 TAA ATA AAA TTT TAA AAA AAG GAA AAA AAA AAA

Fig. 13

196 ACC CGT CTC GGA GCG CTT GCG
thr arg leu gly ala leu ala

217 CTG CCC CGC GGG GAC AGG CCC GGA CGG GCG CCA CCG
leu pro arg gly asp arg pro gly arg ala pro pro

253 GCC GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT
ala ala ser ala arg ala ala arg asn lys arg ala

289 GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG
gly glu glu arg val leu glu lys glu glu glu glu

325 GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC
glu glu glu asp asp glu asp asp asp asp asp asp

361 GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT
val val ser glu gly ser glu val pro glu ser asp

397 CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC
arg pro ala gly ala gln his his gln leu asn **gly**

433 GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC
gly glu arg gly pro gln **thr** ala lys glu arg **ala**

469 AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG
lys glu trp **ser** leu cys gly pro his **pro** gly gln

505 GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC
glu glu gly arg gly pro ala ala gly ser gly thr

541 CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG
arg gln val phe ser met ala ala **leu ser** lys glu

577 GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC
gly gly **ser** ala ser **ser** **thr** thr gly pro asp ser

613 CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC
pro ser pro val pro leu pro pro gly lys pro ala

649 CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT
leu pro gly ala asp gly thr pro phe gly cys pro

Fig. 13 (continued)

685 GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG
 ala gly arg lys glu lys pro **ala** asp pro val glu

721 TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG
 trp thr val met asp val val glu tyr phe thr glu

757 GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG
 ala gly phe pro glu gln ala thr ala phe gln glu

793 CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG
 gln glu ile asp gly lys ser leu leu leu met gln

829 CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG
 arg thr asp val leu thr gly leu ser ile arg leu

865 GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG
 gly pro ala leu lys ile tyr glu his his ile lys

901 GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG
 val leu gln gln gly his phe glu asp asp asp pro

937 GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC
 glu gly phe leu gly

973 CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC
1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG
1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC
1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT
1117 TGC TAC CCC CCC ACC CCG TGT GTG TCT CTG CAC CTG
1153 CCC CCA GCA CAC CCC TCC CGG AGC CTG GAT GTC GCC
1189 TGG GAC TCT GGC CTG CTC ATT TTG CCC CCA GAT CAG
1225 CCC CCT CCC TCC CTC CTG TCC CAG GAC ATT TTT TAA
1261 AAG AAA AAA AGG AAA AAA AAA AAT TGG GGA GGG GGC
1297 TGG GAA GGT GCC CCA AGA TCC TCC TCG GCC CAA CCA
1333 GGT GTT TAT TCC TAT ATA TAT ATA TAT ATG TTT TGT
1369 TCT GCC TGT TTT TCG TTT TTT GGT GCG TGG CCT TTC
1405 TTC CCT CCC ACC ACC ACT CAT GGC CCC AGC CCT GCT
1441 CGC CCT GTC GGC GGG AGC AGC TGG GAA TGG GAG GAG
1477 GGT GGG ACC TTG GGT CTG TCT CCC ACC CTC TCT CCC
1513 GTT GGT TCT GTT GTC GCT CCA GCT GGC TGT ATT GCT
1549 TTT TAA TAT TGC ACC GAA GGG TTG TTT TTT TTT TTT
1585 TAA ATA AAA TTT TAA AAA AAG GAA AAA AAA AAA

Fig. 14

1 GTG GAA AAT AGC AAC TGT GTT TCT CAA GGA TCC AAT
3'7 CCC AAC CTA AGG TGG CAG CGC ACA ATG AAG AAT CAA
met lys asn gln

73 GAC AAA AAG AAC GGG GCT GCC AAA CAG CCC AAC CCC
asp lys lys asn gly ala ala lys gln pro asn pro

109 AAA AGC AGC CCG GGA CAG CCG GAA GCA GGA GCG GAG
lys ser ser pro gly gln pro glu ala gly **ala** glu

145 GGA GCC CAG GGG CGG CCC GGC CGG CCG GCC CCC GCC
gly ala gln **gly** arg pro **gly** **arg** **pro** ala pro ala

181 CGA GAA GCC GAA GGT GCC AGC AGC CAG GCT CCC GGG
arg glu ala glu gly **ala** ser ser gln ala pro **gly**

217 AGG CCG GAG GGG GCT CAA GCC AAA ACT GCT CAG CCT
arg pro glu gly ala gln ala **lys** thr ala gln **pro**

253 GGG GCG CTC TGT GAT GTC TCT GAG GAG CTG AGC CGC
gly ala leu **cys** asp val ser glu glu leu ser arg

289 CAG TTG GAA GAC ATA CTC AGT ACA TAC TGT GTG GAC
gln leu glu asp ile leu ser thr tyr cys val asp

325 AAC AAC CAG GGG GCC CCG GGT GAG GAT GGG GTC CAG
asn asn gln gly **ala** pro gly glu asp gly **val** gln

361 GGT GAG CCC CCT GAA CCT GAA GAT GCA GAG AAG TCT
gly glu pro **pro** glu pro glu asp ala glu lys ser

397 CGC GCC TAT GTG GCA AGG AAT GGG GAG CCG GAG CCG
arg **ala** tyr val ala arg asn gly glu pro glu pro

433 GGC ACC CCA GTA GTC AAT GGC GAG AAG GAG ACC TCC
gly thr pro val val **asn** gly glu lys glu **thr** ser

469 AAG GCA GAG CCG GGC ACG GAA GAG ATC CGG ACG AGC
lys **ala** glu pro **gly** thr glu glu ile arg **thr** ser

505 GAT GAG GTC GGA GAC CGA GAC CAC CGG AGG CCA CAG
asp glu val gly asp arg asp his arg arg pro gln

Fig. 14 (continued)

541 GAA AAG AAG AAG GCC AAG GGT CTG GGA AAG GAG ATC
glu lys lys lys ala lys gly leu gly lys glu ile

577 ACG CTG CTG ATG CAG ACA CTG AAC ACG CTG AGC ACC
thr leu leu met gln thr leu asn thr leu ser thr

613 CCA GAG GAG AAG CTG GCG GCT CTG TGC AAG AAG TAT
pro glu glu lys leu ala ala leu cys lys lys tyr

649 GCG GAA CTG CTC GAG GAG CAC CGG AAC TCG CAG AAG
ala glu leu leu glu glu his arg asn ser gln lys

685 CAG ATG AAG CTG CTG CAG AAG AAG CAG AGC CAG CTG
gln met lys leu leu gln lys lys gln ser gln leu

721 GTG CAG GAG AAG GAC CAC CTG CGT GGC GAG CAC AGC
val gln glu lys asp his leu arg gly glu his ser

757 AAG GCC ATC CTG GCC CGC AGC AAG CTC GAG AGC CTG
lys ala ile leu ala arg ser lys leu glu ser leu

793 TGC CGG GAG CTG CAG CGG CAC AAC CGC TCG CTC AAG
cys arg glu leu gln arg his asn arg ser leu lys

829 GAA GAA GGT GTG CAG CGA GCC CGA GAG GAG GAG GAG
glu glu gly val gln arg ala arg glu glu glu

865 AAG CGC AAG GAG GTG ACG TCA CAC TTC CAG ATG ACG
lys arg lys glu val thr ser his phe gln **met** thr

901 CTC AAC GAC ATT CAG CTG CAG ATG GAG CAG CAC AAC
leu asn asp ile gln leu gln met glu gln his asn

937 GAG CGC AAC TCC AAG CTG CGC CAG GAG AAC ATG GAG
glu arg asn ser lys leu arg gln glu asn met glu

973 CTG GCC GAG CGG CTC AAG AAG CTG ATT GAG CAG TAC
leu ala glu arg leu lys lys leu ile glu gln tyr

1009 GAG CTG CGA GAA GAG CAC ATC GAC AAA GTC TTC AAA
glu leu arg glu glu his ile asp lys val phe lys

Fig. 14 (continued)

1045 CAC AAG GAT CTG CAG CAG CAG CTG GTG GAC GCC AAG
his lys asp leu gln gln gln leu val asp ala lys

1081 CTC CAG CAG GCC CAG GAG ATG CTG AAG GAG GCA GAG
leu gln gln ala gln glu met leu lys glu ala glu

1117 GAG CGG CAC CAG CGG GAG AAG GAC TTT CTC CTG AAG
glu arg his gln arg glu lys asp phe leu leu lys

1153 GAG GCC GTG GAG TCC CAG AGG ATG TGC GAG CTG ATG
glu ala val glu ser gln arg met cys glu leu met

1189 AAG CAA CAG GAG ACC CAC CTG AAG CAG CAG CTT GCC
lys gln gln glu thr his leu lys gln gln leu ala

1225 CTA TAC ACA GAG AAG TTT GAG GAG TTC CAG AAC ACT
leu tyr thr glu lys phe glu glu phe gln asn thr

1261 CTT TCC AAA AGC AGC GAG GTG TTC ACC ACA TTC AAA
leu ser lys ser ser glu val phe thr thr phe lys

1297 CAG GAA ATG GAA AAG ATG ACA AAG AAG ATC AAG AAG
gln glu met glu lys met thr lys lys ile lys lys

1333 CTG GAG AAA GAG ACC ACC ATG TAC CGT TCC CGG TGG
leu glu lys glu thr thr met tyr arg ser arg trp

1369 GAG AGC AGC AAC AAG GCC CTG CTT GAG ATG GCT GAG
glu ser ser asn lys ala leu leu glu met ala glu

1405 GAG AAA ACA CTC CGG GAC AAA GAG CTG GAA GGC CTG
glu lys thr leu arg asp lys glu leu glu gly leu

1441 CAG GTG AAA ATC CAG CGG CTG GAG AAG CTG TGC CGG
gln val lys ile gln arg leu glu lys leu cys arg

1477 GCA CTG CAG ACA GAG CGC AAT GAC CTG AAC AAG AGG
ala leu gln thr glu arg asn asp leu asn lys arg

1513 GTG CAG GAC CTG AGT GCC GGT GGC CAG GGC CCC GTC
val gln asp leu ser ala gly gly gln gly pro val

Fig. 14 (continued)

1549 TCC GAC AGC GGT CCT GAG CGG AGG CCA GAG CCC GCC
ser asp ser gly pro glu arg arg pro **glu pro ala**

1585 ACC ACC TCC AAG GAG CAG GGT GTC GAG GGC CCC GGG
thr thr ser lys glu gln gly val glu gly pro gly

1621 GCT CAA GTA CCC AAC TCT CCA AGG GCC ACA GAC GCT
ala gln **val pro asn ser pro arg ala thr asp ala**

1657 TCC TGC TGC GCA GGT GCA CCC AGC ACA GAG GCA TCA
ser cys cys ala gly ala pro ser thr glu ala ser

1693 GGC CAG ACA GGG CCC CAG GAG CCC ACC ACT GCC ACT
gly gln **thr gly pro gln glu pro thr thr ala thr**

1729 GCC TAG AGA GCT TGG TGC TGG GGT GTG CCA GGA AGG
ala

1765 GAG CAG GCA GCC CAG CCA GGC CTG GCC CAG CCC AGG
1801 CTC CCA TGC TAA GCA GTC CGG TGC TGA GGC CAG GAT
1837 GTT CTG ACC TGG CTG GCA CCT GAC CCT CTG CAG TCT
1873 TGG ATT TTG TGG GTC AGT TTT ACA TGC ATA TGG CAC
1909 ACA TGC AAG GCC TCA CAC ATT TGT GTC TCT AAG TGT
1945 ACT GTG GGC TTG CAT CGG GGG TGA CGA TGG ACA GAT
1981 GAA GCC AGC GGC TCC CTT GTG AGC TGA AGT CTT ACG
2017 GAG GAG ACG GCG TCT GCA CTG CCA TCG CAG TGA CCT
2053 GCA GGA CGA GTT CCT TGA GCT TTC CCT GCC TGC TTT
2089 GAG GCT GAG ACC CCT CCC GGC CCT TCA GAG CTC CTG
2125 ACA GGT GAT ACA CAC CCA GCC TTG ACC GCA CTT CTC
2161 TTG GGT AGC TGG GCT CTC CTA GCC TCC CCC AGA GGC
2197 GCC ATT GCT TCT CTT GAC TTG GAG AGG GGA TGC CCA
2233 GGC GTG GCC TTG GCA GGC ACT GGG AGC TAG TGA TTG
2269 GGC TGC TCT CCT GCC TCG AGC AGG GGC AGG AGT GTT
2305 TCT GGT GGG ATG ATG CGC TCG CTG GTC AGG AGC CCC
2341 GTG GGC GCT GCT TCC CCC GCC CTC TGG TGA TGC CAG
2377 GAC CAG GCC AGT GAT GCT TCT CAG TAG CCT TAC CAT
2413 TCA CAG GTG CCT CTC CAG CCC GCA CAG TGA GTG ACA
2449 AGA TCA TCC AAA GGA TTC CTT CTG AAG GTG TTC GTT
2485 TCG TTT TGT TTT GTT GCA CGT GAC GGT TTG TAT TGA
2521 GGA CCC TCT GAG GAA GAG GGG TGC TGT AGC AGT GGT
2557 CCC TGC GTG CCT GGC TCC AGT GTC CTG CCC TCC CCC
2593 CCC TCG CCA TGG CTC CTC GGC CGC CTT GGT GCT GAG
2629 GTT TCT GTT TGG TGA GAT CAG GTT GTC TGT TCA GAG

Fig. 14 (continued)

2665 AGA AGA GGC GTC TGA TGG CTT TGC CGC CAG CTT GCC
2701 TGC GGG CCT CAA TCC CGG GAG GCC GCC CGG TTC CCG
2737 TCA CTG TTG TCC CCG TGC AGT GCG TTG CTG GTC CCC
2773 AGG ACC AGC TGC TCG TTT GCT GTA TGG GTC AGT TTC
2809 TGC TTC CTG CCC CCC ACT CCA CCT AAC TGC AAT CCT
2845 TGG GGT TTC CCT GGT TCT CGT CCC TGG TAC CTC TGT
2881 GCC CAA GAA GTA GCC TTC TTT GGG ATT CTT GTT CTG
2917 CCC ATG CGG GAG CTG CTG CTG TCT GAC AGG TGA GGC
2953 CTG AGA CTC AGC GGC TGA CAG AGC TGC AGA GCT CTG
2989 CAC GGT GGC TCC CGG GGC GGC CTC TGT GTG CTG CAC
3025 ACC GCT GCT CTG CTG GCA CTG GCC AGT CTG TGC AGA
3061 GCA TTT GAG TAC TGG CTC AGG AGG GAG GGC TCT GCT
3097 GGC CTC GAG GGA CAG CGC CAC GTC TCC AGC TGG GCT
3133 CAG GGA GAG CCC CAG ACT GGC TGC GTA GGG TGC TTG
3169 GGG TTT GCT TCT TGC AGT ATT TCT TGG AAG CTG TTT
3205 TGT TGT CCT GCT ATT CCT TCA TCT TCC ACA GTC CAC
3241 GCT CAG CCT TTA ACT TGG ATC CCT CAC ATA ACA GGG
3277 TTC ATG AGA CCC GCA AGT ACG CCC AAG CTA CGT ATG
3313 GCT GAG GCC AGC TGG CAG GTG AAT GGC ACG CCA TTG
3349 CTG CTG CTA ATC CCT GGC ATA TCT TTA GTT CAC CTC
3385 GAA ATG CCC CCG CCA CAG TGC AAG CAG TGA GTC CAC
3421 GTG CCA CCC TGG GCT GAA TCC CAC CCC CTG TGA GTG
3457 TTG CCC GAG ATT GTG TCT CTT CTG AAT GCC TTC ACT
3493 GGG AAT GGC CTC TGC CGC CTC CTG CTC AGG GAG GCT
3529 TTC CCC TTC CCT CAG CCC CTG TGC CAG ACT GAG GTA
3565 CAA GAA CCG CCA AGC CCA TGC AAG GTG TGG CTA GGC
3601 GCC AGG GTG CAG GAA GGA GGC AGG TAG CTG CCT GCA
3637 CCC TTG AAA GCC AAG AGG CCT ACG GTG GCC TCC ATC
3673 CTG GCT TGC CTC ACT TCA GCT ACC TCG CAT AGC CCA
3709 GGG GTG GGG CTA TTG GAT TCC AGG GTG GGG GGA TGG
3745 GAA GCT GCA GGG GGC AGG TGG CTC TCA CTA GGC TTC
3781 CCA GCT CAG GAA TGT GGG CCT CAG GTA GGG GAG AGC
3817 CTT TGC TCC ACT CCA CCC ATT TGC AGG CAT CTA GGC
3853 CAG TCT AGA TGG CGA CCC CTT CTC TTC CTC TCC ATT
3889 GAC CAA ATC GTA CCT GTC TCT CCA GCT GCT CGC TTG
3925 CTC TGC TTT CCA AAG TCA GCC CAG GTA CCC AGG TGC
3961 CGC CCA CAT TGG CCT GGA ACC TGG ACC AGA GGC AAG
3997 GGA GGT GGC CTA TCC TTG AGT GAT AGC CAG TGC CTT
4033 CCT CAC CCG GTG GCT TCC ATG CCT GTG ACC TCA GAT
4069 TTA GGA CCA AGA GCT GTG TTG GTT TCT TAC GTT GTG
4105 AGC TTT CCC TCC AGG GGA CCA CAG CAG GTG AGG CTC
4141 GGA GCC CAG AGC CCT TGG CGC CGC CAG CAG TAA CTT
4177 GTG TCC GGA CCT TGT CCA GCT GAG CGC TTC GTG TAT

Fig. 14 (continued)

4213 GAC TCA GCT TCG TGT GTG AGT CCA GCG GAG TGC GTC
4249 ACG TGA CCT AGA CTC AGC GGT GTC AGC CGC ACT TTG
4285 ATT TGT TTG TTT TCC ATG AGG TTT TTG GAC CAT GGG
4321 CTT AGC TCA GCC AAC TTT TCT GTA AGG AGA ATG TTA
4357 ACT TTC TGT AAA GAT GCT TAT TTA ACT AAC GCC TGC
4393 TTC CCC CAC TCC CAA CCA GGT GGC CAC CGA GAG CTC
4429 ACC AGG AGG CCA ATA GAG CTG CTC CAG CTC TCC CAT
4465 CTT GCA CCG CAC AAA GGT GGC CGC CCC AGG GAC AGC
4501 CAG GCA CCT GCC TGG GGG AGG GGC TTC TCT TCC TTA
4537 TGG CCT GGC CAT CTA GAT TGT TTA AAG TTG TGC TGA
4573 CAG CTT TTT TTG GTT TTT TGG TTT TTG TTT TTG TTT
4609 TTG TTT TTG TTT TTG TCT ACT TTT GGT ATT CAC AAC
4645 AGC CAG GGA CTT GAT TTT GAT GTA TTT TAA GCC ACA
4681 TTA AAT AAA GAG TCT GTT GCC TTA AAA AAA AAA AAA
4717 AAA AAA

Fig. 15

1 GAC GCC TCA GAG CGG AAC AGG GAA GTG AAT CAG GCG
37 CCG GGT AGT GGG TTG CTG GGC TGG GCT TGC TGA GGT
73 AGA GGC AGC GCC AAG AAG AGG CCT TTG CCG CTG GTC
109 GGG ATT GGG ATG TCG AAG AAC ACA GTG TCG TCG GCC
met ser lys asn thr val ser ser ala

145 CGC TTC CGG AAG GTG GAC GTG GAT GAA TAT GAC GAG
arg phe arg lys val asp val asp glu tyr asp glu

181 AAC AAG TTC GTG GAC GAA GAA GAT GGG GGC GAC GGC
asn lys phe val asp glu glu asp gly gly asp gly

217 CAG GCC GGG CCC GAC GAG GGC GAG GTG GAC TCC TGC
gln ala gly pro asp glu gly glu val asp ser cys

253 CTG CGG CAA GGA AAC ATG ACA GCT GCC CTA CAG GCA
leu arg gln gly asn met thr ala ala leu gln ala

289 GCT CTG AAG AAC CCC CCT ATC AAC ACC AAG AGT CAG
ala leu lys asn pro pro ile asn thr **lys** ser gln

325 GCA GTG AAG GAC CGG GCA GGC AGC ATT GTC TTG AAG
ala val lys asp arg ala gly ser ile val leu lys

361 GTG CTC ATC TCT TTT AAA GCT AAT GAT ATA GAA AAG
val leu ile ser phe lys ala **asn** asp ile glu lys

397 GCA GTT CAA TCT CTG GAC AAG AAT GGT GTG GAT CTC
ala val gln ser leu asp **lys** asn gly val asp leu

433 CTA ATG AAG TAT ATT TAT AAA GGA TTT GAG AGC CCG
leu met lys tyr ile tyr lys gly phe glu ser pro

469 TCT GAC AAT AGC AGT GCT ATG TTA CTG CAA TGG CAT
ser asp asn ser ser ala **met** leu leu gln trp his

505 GAA AAG GCA CTT GCT GCT GGA GGA GTA GGG TCC ATT
glu lys ala leu ala ala gly gly val gly ser ile

541 GTT CGT GTC TTG ACT GCA AGA AAA ACT GTG TAG TCT
val arg val leu thr ala arg lys thr val

Fig. 15 (continued)

577 GGC AGG AAG TGG ATT ATC TGC CTC GGG AGT GGG AAT
613 TGC TGG TAC AAA GAC CAA AAC AAC CAA ATG CCA CCG
649 CTG CCC TGT GGG TAG CAT CTG TTT CTC TCA GCT TTG
685 CCT TCT TGC TTT TTC ATA TCT GTA AAG AAA AAA ATT
721 ACA TAT CAG TTG TCC CTT TAA TGA AAA TTG GGA TAA
757 TAT AGA AGA AAT TGT GTT AAA ATA GAA GTG TTT CAT
793 CCT TTC AAA ACC ATT TCA GTG ATG TTT ATA CCA ATC
829 TGT ATA TAG TAT AAT TTA CAT TCA AGT TTT AAT TGT
865 GCA ACT TTT AAC CCT GTT GGC TGG TTT TTG GTT CTG
901 TTT GGT TTT GTA TTA TTT TTA ACT AAT ACT GAA AAA
937 TTT GGT CAG AAT TTG AGG CCA GTT TCC TAG CTC ATT
973 GCT AGT CAG GAA ATG ATA TTT ATA AAA AAT ATG AGA
1009 GAC TGG CAG CTA TTA ACA TTG CAA AAC TGG ACC ATA
1045 TTT CCC TTA TTT AAT AAG CAA AAT ATG TTT TTG GAA
1081 TAA GTG GTG GGT GAA TAC CAC TGC TAA GTT ATA GCT
1117 TTG TTT TTG CTT GCC TCC TCA TTA TCT GTA CTG TGG
1153 GTT TAA GTA TGC TAC TTT CTC TCA GCA TCC AAT AAT
1189 CAT GGC CCC TCA ATT TAT TTG TGG TCA CGC AGG GTT
1225 CAG AGC AAG AAG TCT TGC TTT ATA CAA ATG TAT CCA
1261 TAA AAT ATC AGA GCT TGT TGG GCA TGA ACA TCA AAC
1297 TTT TGT TCC ACT AAT ATG GCT CTG TTT GGA AAA AAC
1333 TGC AAA TCA GAA AGA ATG ATT TGC AGA AAG AAA GAA
1369 AAA CTA TGG TGT AAT TTA AAC TCT GGG CAG CCT CTG
1405 AAT GAA ATG CTA CTT TCT TTA GAA ATA TAA TAG CTG
1441 CCT TAG ACA TTA TGA GGT ATA CAA CTA GTA TTT AAG
1477 ATA CCA TTT AAT ATG CCC CGT AAA TGT CTT CAG TGT
1513 TCT TCA GGG TAG TTG GGA TCT CAA AAG ATT TGG TTC
1549 AGA TCC AAA CAA ATA CAC ATT CTG TGT TTT AGC TCA
1585 GTG TTT TCT AAA AAA AGA AAC TGC CAC ACA GCA AAA
1621 AAT TGT TTA CTT TGT TGG ACA AAC CAA ATC AGT TCT
1657 CAA AAA ATG ACC GGT GCT TAT AAA AAG TTA TAA ATA
1693 TCG AGT AGC TCT AAA ACA AAC CAC CTG ACC AAG AGG
1729 GAA GTG AGC TTG TGC TTA GTA TTT ACA TTG GAT GCC
1765 AGT TTT GTA ATC ACT GAC TTA TGT GCA AAC TGG TGC
1801 AGA AAT TCT ATA AAC TCT TTG CTG TTT TTG ATA CCT
1837 GCT TTT TGT TTC ATT TTG TTT TGT TTT GTA AAA ATG
1873 ATA AAA CTT CAG AAA ATA AAA TGT CAG TGT TGA ATA
1909 ATT AAA AAA AAA AAA AA

Fig. 16

1 GAA GAG CGA GTA CTT GAG AAA GAA GAG GAA GAA GAT
glu glu arg val leu glu lys glu glu glu glu **asp**

37 GAT GAT GAA GAT GAA GAT GAA GAT GAT GTG TCA
asp **asp** glu asp **glu** **asp** **glu** **asp** asp asp val ser

73 GAG GGC TCT GAA GTG CCC GAG AGT GAC CGT CCT GCA
glu gly ser glu val pro glu ser asp arg pro ala

109 GGT GCC CAG CAC CAC CAG CTT AAC GGC GAG CGG GGA
gly ala gln his his gln leu asn gly glu arg gly

145 CCT CAG AGT GCC AAG GAG AGG GTC AAG GAG TGG ACC
pro gln **ser** ala lys glu arg **val** lys glu trp **thr**

181 CCC TGC GGA CCG CAC CAG GGC CAG GAT GAA GGG CGG
pro cys gly pro his **gln** gly gln **asp** glu gly arg

217 GGG CCA GCC CCG GGC AGC GGC ACC CGC CAG GTG TTC
gly pro ala **pro** gly ser gly thr arg gln val phe

253 TCC ATG GCA GCC ATG AAC AAG GAA GGG GGA ACA GCT
ser met ala ala **met** **asn** lys glu gly gly **thr** ala

289 TCT GTT GCC ACC GGG CCA GAC TCC CCG TCC CCC GTG
ser **val** **ala** thr gly pro asp ser pro ser pro val

325 CCT TTG CCC CCA GGC AAA CCA GCC CTA CCT GGG GCC
pro leu pro pro gly lys pro ala leu pro gly ala

361 GAC GGG ACC CCC TTT GGC TGT CCT CCC GGG CGC AAA
asp gly thr pro phe gly cys pro **pro** gly arg lys

397 GAG AAG CCA TCT GAT CCC GTC GAG TGG ACC GTG ATG
glu lys pro **ser** asp pro val glu trp thr val met

433 GAT GTC GTC GAA TAT TTT ACT GAG GCT GGA TTC CCG
asp val val glu tyr phe thr glu ala gly phe pro

469 GAG CAG GCG ACA GCT TTC CAA GAG CAG GAA ATT GAT
glu gln ala thr ala phe gln glu gln glu ile asp

Fig. 16 (continued)

505 GGC AAA TCT TTG CTG CTC ATG CAG CGC ACA GAT GTG
gly lys ser leu leu leu met gln arg thr asp val

541 CTC ACC GGC CTG TCC ATC CGC CTC GGG CCA GCC CTG
leu thr gly leu ser ile arg leu gly pro ala leu

577 AAA ATC TAC GAG CAC CAC ATC AAG GTG CTT CAG CAA
lys ile tyr glu his his ile lys val leu gln gln

613 GGC CAC TTT GAG GAT GAT GAC CCC GAT GGC TTC TTA
gly his phe glu asp asp asp pro **asp** gly phe leu

649 GGC TGA GCG CCC AGC CTC ACC CCT GCC CCA GCC CAT
gly

685 TCC GGC CCC CAT CTC ACC CAA GAT CCC CCA GAG TCC
721 AGG AGC TGG ACG GGG ACA CCC TCA GCC CTC ATA ACA
757 GAT TCC AAG GAG AGG GCA CCC TCT TGT CCT TAT CTT
793 TGC CCC TTG TNT CTG TCT CAC ACA CAT CTG CTC CTC
829 AGC ACG TCG GTG TGG GGA GGG GAT TGC TCC TTA AAC
865 CCC AGG TGG CTG ACC CTC CCC ACC CAG TCC AGG ACA
901 TTT TAG GAA AAA AAA AAT GAA ATG TGG GGG GCT TCT
937 CAT CTC CCC AAG ATC CTC TTC CGT TCA GCC AGA TGT
973 TTC CTG TAT AAA TGT TTG GAT CTG CCT GTT TAT TTT
1009 GGT GGG TGG TCT TTC CTC CCT CCC CTA CCA CCC ATG
1045 CCC CCC TTC TCA GTC TGC CCC TGG CCT CCA GCC CCT
1081 AGG GGA CTA GCT GGG TTG GGG TTC CTC GGG CCT TTT
1117 CTC TCC TCC CTC TTT TCT TTC TGT TGA TTG TCG CTC
1153 CAG CTG GCT GTA TTG CTT TTT AAT ATT GCA CCG AAG
1189 GTT TTT TAA ATA AAA TTT TA

Fig. 17

1 CA AAA AGC AGC CCA GGA CAA CCG GAA GCA GGA CCC GAG GGA GCC
lys ser ser pro gly gln pro glu ala gly pro glu gly ala

45 CAG GAG CGG CCC AGC CAG GCG GCT CCT GCA GTA GAA GCA GAA GGT
gln glu arg pro ser gln ala ala pro ala val glu ala glu gly

90 CCC GGC AGC AGC CAG GCT CCT CGG AAG CCG GAG GGG GCT CAA GCC
pro gly ser ser gln ala pro arg lys pro glu gly ala gln ala

135 AGA ACG GCT CAG TCT GGG GCC CTT CGT GAT GTC TCT GAG GAG CTG
arg thr ala gln ser gly ala leu arg asp val ser glu glu leu

180 AGC CGC CAA CTG GAA GAC ATA CTG AGC ACA TAC TGT GTG GAC AAT
ser arg gln leu glu asp ile leu ser thr tyr cys val asp asn

225 AAC CAG GGG GGC CCC GGC GAG GAT GGG GCA CAG GGT GAG CCG GCT
asn gln gly pro gly glu asp gly ala gln gly glu pro ala

270 GAA CCC GAA GAT GCA GAG AAG TCC CGG ACC TAT GTG GCA AGG AAT
glu pro glu asp ala glu lys ser arg thr tyr val ala arg asn

315 GGG GAG CCT GAA CCA ACT CCA GTA GTC TAT GGA GAG AAG GAA CCC
gly glu pro glu pro thr pro val val tyr gly glu lys glu pro

360 TCC AAG GGG GAT CCA AAC ACA GAA GAG ATC CGG CAG AGT GAC GAG
ser lys gly asp pro asn thr glu glu ile arg gln ser asp glu

405 GTC GGA GAC CGA GAC CAT CGA AGG CCA CAG GAG AAG AAA AAA GCC
val gly asp arg asp his arg arg pro gln glu lys lys ala

450 AAG GGT TTG GGG AAG GAG ATC ACG TTG CTG ATG CAG ACA TTG AAT
lys gly leu gly lys glu ile thr leu leu met gln thr leu asn

495 ACT CTG AGT ACC CCA GAG GAG AAG CTG GCT GCT CTG TGC AAG AAG
thr leu ser thr pro glu glu lys leu ala ala leu cys lys lys

540 TAT GCT GAA CTG CTG GAG GAG CAC CGG AAT TCA CAG AAG CAG ATG
tyr ala glu leu leu glu his arg asn ser gln lys gln met

585 AAG CTC CTA CAG AAA AAG CAG AGC CAG CTG GTG CAA GAG AAG GAC
lys leu leu gln lys gln ser gln leu val gln glu lys asp

630 CAC CTG CGC GGT GAG CAC AGC AAG GCC GTC CTG GCC CGC AGC AAG
his leu arg gly glu his ser lys ala val leu ala arg ser lys

675 CTT GAG AGC CTA TGC CGT GAG CTG CAG CGG CAC AAC CGC TCC CTC
leu glu ser leu cys arg glu leu gln arg his asn arg ser leu

Fig. 17 (continued)

720 AAG GAA GAA GGT GTG CAG CGG GCC CGG GAG GAG GAG AAG CGC
lys glu glu gly val gln arg ala arg glu glu glu lys arg

765 AAG GAG GTG ACC TCG CAC TTC CAG GTG ACA CTG AAT GAC ATT CAG
lys glu val thr ser his phe gln val thr leu asn asp ile gln

810 CTG CAG ATG GAA CAG CAC AAT GAG CGC AAC TCC AAG CTG CGC CAA
leu gln met glu gln his asn glu arg asn ser lys leu arg gln

855 GAG AAC ATG GAG CTG GCT GAG AGG CTC AAG AAG CTG ATT GAG CAG
glu asn met glu leu ala glu arg leu lys lys leu ile glu gln

900 TAT GAG CTG CGC GAG GAG CAT ATC GAC AAA GTC TTC AAA CAC AAG
tyr glu leu arg glu glu his ile asp lys val phe lys his lys

945 GAC CTA CAA CAG CAG CTG GTG GAT GCC AAG CTC CAG CAG GCC CAG
asp leu gln gln leu val asp ala lys leu gln gln ala gln

990 GAG ATG CTA AAG GAG GCA GAA GAG CGG CAC CAG CGG GAG AAG GAT
glu met leu lys glu ala glu glu arg his gln arg glu lys asp

1035 TTT CTC CTG AAA GAG GCA GTA GAG TCC CAG AGG ATG TGT GAG CTG
phe leu leu lys glu ala val glu ser gln arg met cys glu leu

1080 ATG AAG CAG CAA GAG ACC CAC CTG AAG CAA CAG CTT GCC CTA TAC
met lys gln gln glu thr his leu lys gln gln leu ala leu tyr

1125 ACA GAG AAG TTT GAG GAG TTC CAG AAC ACA CTT TCC AAA AGC AGC
thr glu lys phe glu glu phe gln asn thr leu ser lys ser ser

1170 GAG GTA TTC ACC ACA TTC AAG CAG GAG ATG GAA AAG ATG ACT AAG
glu val phe thr thr phe lys gln glu met glu lys met thr lys

1215 AAG ATC AAG AAG CTG GAG AAA GAA ACC ACC ATG TAC CGG TCC CGG
lys ile lys leu glu lys glu thr thr met tyr arg ser arg

1260 TGG GAG AGC AGC AAC AAG GCC CTG CTT GAG ATG GCT GAG GAG AAA
trp glu ser ser asn lys ala leu leu glu met ala glu glu lys

1305 ACA GTC CGG GAT AAA GAA CTG GAG GGC CTG CAG GTA AAA ATC CAA
thr val arg asp lys glu leu glu gly leu gln val lys ile gln

1350 CGG CTG GAG AAG CTG TGC CGG GCA CTG CAG ACA GAG CGC AAT GAC
arg leu glu lys leu cys arg ala leu gln thr glu arg asn asp

1395 CTG AAC AAG AGG GTA CAG GAC CTG AGT GCT GGT GGC CAG GGC TCC
leu asn lys arg val gln asp leu ser ala gly gly gln gly ser

1440 CTC ACT GAC AGT GGC CCT GAG AGG CCA GAG GGG CCT GGG GCT
leu thr asp ser gly pro glu arg arg pro glu gly pro gly ala

Fig. 17 (continued)

1485 CAA GCA CCC AGC TCC CCC AGG GTC ACA GAA GCG CCT TGC TAC CCA
gln ala pro ser ser pro 'arg val thr glu ala pro cys tyr pro

1530 GGA GCA CCG AGC ACA GAA GCA TCA GGC CAG ACT GGG CCT CAA GAG
gly ala pro ser thr glu ala ser gly gln thr gly pro gln glu

1575 CCC ACC TCC GCC AGG GCC TAG AGA GCC TGG TGT TGG GTC ATG CTG
pro thr ser ala arg ala ***

1620 GGA AGG GAG CGG CAG CCC AGC CAG GCC TGG CCC ATA AAA GGC TCC
1665 CAT GCT GAG CAG CCC ATT GCT GAA GCC AGG ATG TTC TTG ACC TGG
1710 CTG GCA TCT GGC ACT TGC AAT TTT GGA TTT TGT GGG TCA GTT TTA
1755 CGT ACA TAG GGC ATT TTG CAA GGC CTT GCA AAT GCA TTT ATA CCT
1800 GTA AGT GTA CAG TGG GCT TGC ATT GGG GAT GGG GGT GTG TAC AGA
1845 TGA AGT CAG TGG CTT GTC TGT GAG CTG AAG AGT CTT GAG AGG GGC
1890 TGT CAT CTG TAG CTG CCA TCA CAG TGA GTT GGC AGA AGT GAC TTG
1935 AGC ATT TCT CTG TCT GAT TTG AGG CTC AGA CCC CTC CCT GCC CTT
1980 TCA GAG CTC AAA ACA AGT AAT ACA CCA AGG TCT TGA CTG CAT TTG
2025 TCT TGT GAG CAG GGC TTG CTT GGT CAG CTC AGG CCC TCC TAG CTG
2070 CTT GGA GGC TCC TTT GAT TCT CTA GAC CTG GAA AAG GTG TCC CTA
2115 GGC AGA GCC CTG GCA GGG CGC TCA GAG CTG GGA TTT CCT GCC TGG
2160 AAC AAG GGA CCT GGA GAA TGT TTT TGC GTG GGA TGA TGT GCT GGT
2205 CAG GAG CCC CTT GGG CAT CGC TTC CCC TGC CCT TTG GTA GTG CCA
2250 GGA CCA GGC CAA TGA TGC TTC TCA GTA GCC TTA TCA TTC ACA GGT
2295 GCC TCT CTA GCC TGC ACA AAT GAT TGA CAA GAG ATC ACC CAA AGG
2340 ATT ATT TCT GAA GGT GTT TTT TTC TTT ATT TCT TTT TCT TTT TTT
2385 TTT TTT CTT TTT CTT TTT TTG CAC ATG ACA GTG TTT GTA TTG
2430 AGG ACC TTC CAA GGA AAA GGG ATG CTG TAC CAG TGG TGC CTG GGT
2475 GCC TGG CCT CCA GTG TCC CAC CTC CTT CAC CAC CCC ACT TGG CTC
2520 CTT TGC CAT CTT GAT GCT GAG GTT TCC TGT TTG GTG AGA TCA GGT
2565 TGT TTG TGG TAA AAG AAA GGA AAG GGC TTC TGA TGG CTT TGC CAC
2610 AAG CTT ACC TGT GGG TTT CAG TCC TGA GAG GCC ACC ACC AGT TCC
2655 CAT CAG CAC TGT CTC CAT GCA GCA GTT GCT GGG TCC CAT GTC CAG
2700 CTG CCT CTT TGG CTT CAT GGG TTT TTC TGC TTC CTG CCC CCA CCC
2745 CCA CAT GTG CAA TCC TCA AGA TTT GTC CTG ATT CTA TTT CCT GGC
2790 ACC TCC CTG CCT GTC CTT GGG GAT TCT ACT TCT TCC TGT GTG GGG
2835 CCC ATA GCT GTT GTC TAA CAG GTA AGA AAT GAA ATT GAA CTA TTG
2880 ACT GGG CCC CAG AAA TCC ATA AAA TGG CTG CAG ACA GTT GTT TCT
2925 GTG TCC TGT TCT ACC CCC ACT CCA GTA CAT AAC TAC TAT GTA CTG
2970 TGT AGA GCC ATT CTA TAT GCT GAA TGT TCT GCT GTT GCA AAC TTG
3015 CCA GGG TAT TAG CCA GTG TTT GTG CCA AGC AGT TTT CGG GGA CAA
3060 CAG AAT GAC TCA GAC CAA GAT GGA TAG GAT GGT TAG GGC TTT GCT
3105 TCT TGC TGT TTT TCT TTG AAC TAG TCA TTG TCC TGC AGG TCC CTT
3150 CAT CTT CCA TAC CTA GCC CAC TCT TTT AGC CCT TAC CTT AAA TCT
3195 CTC AGA TAA GTT GGT TCA CAA AGA ATG TTA AGT ACT GAA TCA TGT
3240 GTG ACT GAG ACC AGA GAT GGC AAA TGA ATG GCA CAC CAT TTC TCC
3285 TTC TCC TGC CCC AGG GCA GGT ACC ACT GAT CTG CAT CAG AGT TGC
3330 CTG CTA TTC TCT GGT GTA TCC TTC ACA TCT AGG TGC CCT CAA GCA
3375 GCT GTG TGA GTG TTG AGA TCT CTG CCA TCT CTG GCT GAG ATA CTG
3420 CTG TCC TGT GAA GTG TTT CCC ATG ACC TTT TTC TCC CCC TTT GAA
3465 TCC CTC TTG TCT GGA GTA GTC CTT GCC TTC TTG CTC CAG TAG

Fig. 17 (continued)

3510 GCC TTT TCC TTA CCC CAG CCC TTG TGC CAG GCT AAG CTG GTA CAA
3555 GAG CTG CCA ACT CAC AGA GTT TTG CTA GGC GAG AGA GGT GCA GGG
3600 AAG AGG CAG AGG TAT GCA CCT TCC CCC TTG AAG AGA GGG GAA AGG
3645 CCT ACA GTG GCC CAC ATA ATT GCC TGA CTC ACA CTT CAG CTA CCT
3690 CTT AAT GCC TGT GGA GGG ACT GGA GCT GCT GGA TCC CAG TGT GGT
3735 GGT GTA GGA GGC CAC AGT GAG CAG GTG GCC CCA GCT GGG TTT CCC
3780 AGG TCA GGA ATG TGG GCC CCA GGC AAG GTG CAG CCT TTG CTC ACA
3825 GCT CCA TCC ATG TCT AGA CCT TCA GGC CAG TCT GCA GAT GAG GTT
3870 CCC TAC CTT TTT CTT CTC TTC ATT GAC CAA ATC AAC CAA TCA CTA
3915 CAG CTG CTC TGC TTC TGC TTT CCA AAG TAG CCC AGG TCC TGG GCC
3960 AGA TGC AGG GGA GGT GCC TAT CCA TGA GTG AAG GCC AGT GTC TTC
4005 CTC ACC TGG GTG GTC CCA CAC TTG TGA CCC TCA GTT TTA GGA CCC
4050 AAG ATC TGT GTT GGT TTC TTA GAT TGC TAG CTT TTC CTC CAG GGG
4095 ACC ACA GCA GGT GAA GCT CAA GAG CGC ATG GCT CTG CTA ATA GTA
4140 AAT TGT TTT CAG GGC CTT GTC CAG CTG AGA GCT TCA TGT CCA CCA
4185 GAT TCT GAG AGG TGT CAG CAG CAC TTT TTT TTT TTA TTT GTT GTT
4230 TGT TTT CCA TGA GGT TAT CGG ACC ATG GGC TGA GCT CAG GCA CTT
4275 TCT GTA GGA GAC TGT TAT TTC TGT AAA GAT GGT TAT TTA ACC CTC
4320 CTC CAC CCC ATC ACG GTG GCC CTG AGG GCT GAC CCG GAG GCC AGT
4365 GGA GCT GCC TGG TGT CCA CGG GGG AGG GCC AAG GCC TGC TGA GCT
4410 GAT TCT CCA GCT GCT GCC CCA GCC TTT CCG CCT TGC ACA GCA CAG
4455 AGG TGG TCA CCC CAG GGA CAG CCA GGC ACC TGC TCC TCT TGC CCT
4500 TCC TGG GGG AAA GGA GCT GCC TTC TGT CCC TGT AAC TGC TTT CCT
4545 TAT GGC CCA ACC CGG CCA CTC AGA CTT GTT TGA AGC TGC ACT GGC
4590 AGC TTT TTT GTC TCC TTT GGG TAT TCA CAA CAG CCA GGG ACT TGA
4635 TTT TGA TGT ATT TTA AAC CAC ATT AAA TAA AGA GTC TGT TGC CTT
4680 AAA AAA AAA AAA AAA AAA

Fig. 18

GTG GAC GTG GAT GAG TAC GAC GAG AAC AAG TTC GTG
val asp val asp glu tyr asp glu asn lys phe val

GAC GAG GAA GAC GGC GGC GAC GGC
asp glu glu asp gly gly asp gly

Fig. 19

Rabbit	MSKNTVSSAR FRKVDVDEYD ENKFVDEEDG GDGQAGPDEG EVDSCLRQGN	50
Human
Rabbit	MTAALQAALK NPPINTRSQA VKDRAGSIVL KVLISFKAGD IEKAVQSLDR	100
Human K..... N..... K	
Rabbit	NGVDLLMKYI YKGFEPSDN SSAVLLQWHE KALAAGGVGS IVRVLTARKT	150
Human M.....	
Rabbit	V	151
Human	.	

Fig. 20

Rabbit	EERVLEKEEEE EEEEEEDEDDE DDVVSEGSE VPESDRPAGA QHHQLNNGGER	50
HumanDDD..EDEE	
Rabbit	GPQTAKERAK EWSLCGPHPG QEEGRGPAAG SGTRQVFSMA ALSKEGGSAS	100
Human	...S....V. ...TP....Q. .D.....P.MN....T..	
Rabbit	STTGPDSPSP VPLPPGKPAL PGADGTPFGC PAGRKEKPAD PVEWTVMDDVV	150
Human	VA.....P.....S.	
Rabbit	EYFTEAGFPE QATAFQEQEII DGKSLLLLMQR TDVLTGLSIR LGPALKIYEH	200
Human	
Rabbit	HIKVLOQQGHF EDDDPPEGFLG	220
Human D....	

Fig. 21

Rabbit	MKNQDKKNGA AKQPNPKSSP GQPEAGAEGA QGRPGRPAPA REAEG-ASSQ	50
Human	----- P... E.. SQA... V....PG...	
Rabbit	APGRPEGAAQA KTAQPGALCD VSEELSRQLE DILSTYCVDN NQGAPGEDGV	100
Human	..RK..... R...S...R.G.....A	
Rabbit	QGEPPPEPEDA EKSRAYVARN GEPEPGTPVV NGEKETSKAE PGTEEIRTSD	150
HumanA..... .T..... -.... Y....P..GD .N.....Q..	
Rabbit	EVGDRDHRRP QEKKAKGLG KEITLLMQTL NTLSTPEEKL AALCKKYAEL	200
Human	
Rabbit	LEEHRSNSQKQ MKLLQKKQSQ LVQEKDHLRG EHSHKAILARS KLESLCRELQ	250
Human V.....	
Rabbit	RHNRSLSKEEG VQRAREEEEK RKEVTSHFQM TLNDIQLQME QHNERNSKLR	300
Human V	
Rabbit	QENMELAERL KKLIEQYELR EEHIDKVFKH KDLQQQLVDA KLQQAQEMLK	350
Human	
Rabbit	EAEERHQREK DFLLKEAVES QRMCELMKQQ ETHLKQQLAL YTEKFEEFQN	400
Human	
Rabbit	TLSKSSEVFT TFKQEMEKMT KKIKKLEKET TMYRSRWESS NKALLEMAEE	450
Human	
Rabbit	KTLRDKELEG LQVKIQRLEK LCRALQTERN DLNKRVQDLS AGGQGPVSDS	500
Human	..V..... SLT..	
Rabbit	GPERRPEPAT TSKEQGVVEGP GAQVPNSPRA TDASCCAGAP STEASGQTGP	550
Human A.S...V .E.P.YP...	
Rabbit	QEPTTATA	551
HumanS.R.	

Fig. 22 (1/5)

1	AAGCTTTATAAAGATTTACTACCTAATAAGGTAGAGAAGTAATTATGTGCCACTAAA	60
61	AAATACTCAATTCTGAATGTCGCCCCAAATTAACTTGTCACTCATTAAATCATTGAC	120
121	TAGAAACACGTTGAGTACCTATTATGTACTAGGCACCTAGATCATTGTGAGACAATAAAA	180
181	AATACTGCATTAGAAAAGGACATTTCACATCTTAAATGCAATAAGCATTTGGCTG	240
241	GCAGTTAATTACATTAAACACATTAACATATAGAGCAAAATTCTGAGCAATCAAATAAA	300
301	TTATACCCCTTGAGCAATCGATTATTAAATTCTTCACTATTCCCTTAAGCTGATTCT	360
361	ACTCTGGGATTCTTCATAGTTCTCAAATAAGAAAATAAAAATTCTCAAATAAGGCAA	420
421	TACAAAAGAATAGAAATGTAAGAGAAGAGATATTAGCTCTGAAATCCCTGTTCCATT	480
481	TGCTGTCAATAGTGCCTCTAATGTCGATTTCTCTCAAAGAAAAATCTGATTAAAAA	540
541	GGAAAGAAAAAGTACAATCACCTTAAACAGCTAAAGTATACTGATTAGCATCTACTAAAGT	600
601	TAGCAAAGACTGAAACTGAAAAAAATTGTAATACTTATTCTAAAGTTATATAACGCCA	660
661	TTCACCATAGTAATGATTTATACTTGGTATATGGCTTTAAAATAAATATTGCCAAC	720
721	AGGAAAAAAATTTCCTTGTGCTCTAAGGCATTCTAAAGAGAATTTTACCAGTGTGT	780
781	GTCATAACTGAATGTAATTAAACATGTTACTTCTATCACCTAAATGATATACTTA	840
841	TAGAAGAGTGTAAATTGGAACAGAAAAACACCACATTGCTTCTCCCAGAAAAAGG	900
901	GATGTATTCCATTCTCGAGGTCTCTCTCCCACCTCTCTATTATATAATACTGCATA	960
961	GATAAATATACACACATTATATATGTTATTGAACTTAAAGAAGACTGGACATATGT	1020
1021	ATTACATGTATATATCCAACAAATTAAATTGAGATCTCTCCCTCTGATT	1080
1081	ATTATTCTCAGTATGAAATTCTCAAACACTGTACGGTCTTACATTTCTTCATTCACTCAG	1140
1141	CATGTATCGAGTCCCTCTGCATGCTTAGCTTTGTCATATGAAAGGAAGATACAAAAG	1200
1201	AAAAACTGTTCTGCCCTTCAGAACATTCTTCATCTCTAGGAAGGAGATAAACACCA	1260
1261	TATATCATTAAAGAAATTATAAGACTAGTCCAAAACCAATGGTACAAGCAACATGCATT	1320
1321	TTACATTATGAGAATTAGAGCTTGGAAACACTTCTGTATATAATCTTAAGAAC	1380
1381	AATCTTGTAAAGTGCACATTATTAGCTCCATTCTCAGTGTGAGGAATCTGAGACAGAATT	1440
1441	TTAAGTGACATGTCTCGTCAAACATTATGAGTGGAAAGAGTCAACACTTAAGCTGAGTT	1500
1501	TTCTGATTCTAAGCCTAGTGTCTTCAACACAGCACTGGAAACCAAAGATTGTGGTAC	1560
1561	ACAACAAGGCAACAGCCAGTCTTGTGAGGTCAACTAAACTGGACCCATACCGAG	1620
1621	CAGTGTCCAGGCAAATGTCAAATTAAATTCTCGCAAATATTGTTCTCAGTGTAA	1680
1681	TACACACAGCACAACCTACCAATTCTCGTCTAGTGCCTTATCTCCTACATCCAGAA	1740
1741	ATGGGGATGTCAAATATTGTTAAATCTGGCCTAGATGGAATCATATAATCTCAAATC	1800
1801	ATAATATAAACTTAAAGGTCTGGTTCCACCAATCCTCACATTGTTTCCCCCAG	1860
1861	CACTAGAGAGCCTAACCTACCCCTACCCCTGGCAGCATTCTGCTCCAAACGACCACCT	1920
1921	ATTAAAGATGTCATGACCCCTTCCCAAATTCTACAAATTCAACCCAGTTTGCCACCC	1980
1981	GACCCCAGCGCTGCCCGGACACGTTCCCTCCCTCCAAATAGATTGATACCGAGTTCA	2040
2041	GGTCTGCAGATCCCGTGTGCGATGCTGTCACACAGCACTGACAGATAAGATTGACCTT	2100
2101	CGACTCCGTCTGGGACTTCCCGCTGGCAAAGAAGGGTAGTCCAATCCCAGGAAACG	2160
2161	GGCTTCCCTGCTCAGGAACGCGACGCTCTAGCAGCGCACAGTGTGAGGCAATGTCTCCGGCA	2220
2221	ATTAGAACGATGCTGGCGCCGGGTGTGCATCACTCTGCCCTCATACTCCTACCAACTGC	2280
2281	AGGGCACTCGGTCCGGCAGCCAGTCCATCCCACCCACACCCAAGTCCAGGCCAGCGGAC	2340
2341	CTTACGCAGGACCCCGATGATAGGTGCTGACGGCTGCGCAAAGCCAAGGCCACCTGC	2400
2401	CGCTGCTGCCCATCCCCGCAATCTGAGACCCCTAGACTGGACCCAGAAAAGCGTTTC	2460
2461	TATGGGAACCCCCCACCAGAGAATCACGTGACGCAATCGGACGACCAATCGCTCTTACC	2520
2521	TCTGCCCGCGGTCCAGCTTGGCCTCCCTCGCCCCCGCTCCCTCGCCCGAGCCCCG	2580
2581	CCCCCTGCCTGCGAGAGGCCGCGCTGCGCGCTGTGTCCTGCGCGCTCTCCCTCGCG	2640
2641	CGCGCTCTCCGTGGAAGAGCAGGGCAGCGTGGAGGCCAAGGGAGCGCGAACCTGAG	2700
2701	GAGGAAGAAACGGGCTAGCGCGCAGGCCAGAACGGTCCGAGGCCGGCAGTCGGCGAC	2760
2761	GCCTCAGAGCGGAAGAGGAAAGTGAATCAGGGCGCCGGTAGTGGGTGCTGGCTGGGCT	2820
2821	TGCTGAGGTAGAGGCAGCGCCAAGAAGAGGCCTTGCCTGGTGGGATTGGGATGTCG	2880
	M S	
2881	AAGAACACAGTGTGTCGGCCCCGCTTCCGGAAAGGTGGACGTGGATGAATATGACGAGAAC	2940
	K N T V S S A R F R K V D V D E Y D E N	

Fig. 22 (continued; 2/5)

2941	AAGTCGTGGACGAAGAAGATGGGGCGACGCCAGGCCGCCCCACGAGGGCGAGGTG K F V D E E D G G D G Q A G P D E G E V	3000
3001	GACTCCTGCCTCGGGCAATATCCTGCATTACGCCCTCCCCACCCCAGCCCAGCCCAG D S C L R Q	3060
3061	CCCGCCCTTCTGGGACCCGGGAGCCTGCAGGATCCGGGGCACCGCGCGGAGCTG 3121 CCTCTCAACCTGCAGCTTAACCTGTCTCTTGGATGCCCGCTCTGAGAGGGCAAGGGG 3181 GAAGCCCCCGTTCTACCCAGTCGGCAGGAGACCGCAGGGTCCACTCTTGAAGCCTG 3241 CCCTACCCCGCGCCTCCACGCCCCCAGATTCTCAGGTTGCACCCGAGTGCCTGCCT 3301 GCCTCGGGAACTGGTCCCAGCCGCCCCCTCGCGCGCTGGGAAGGCGGGCCCGGCT 3361 GGTGGGGAAAGGCTGGTCCGACCCCTTAGTTTCTCCTAGAACCTGTGATTTCCTGGG 3421 GTCAACATTAGCTCCAGAAATTCTGATTGTGGGAAACCTGCATCTTCCTTAGTGGTTT 3481 GTTTTTGGTTGTGTTTGTTATTGGTAGCGTTAAGGTAGTTATTGCTTACCGGGGGG 3541 CCGGGGGAGATGGGACTGTCGAAAATTGAGGGTCCCTGTGCTTCAGCCCATTGGCCT 3601 TTAAAAAAAGAAGAAGAAGAAGAGGGATTGGCAAATATACATTGTACAG 3661 AATTGTTAATGGGGAGGGGAATGAATACAAAAAATACAAAATCCTAGAAGGAAGCT 3721 TGAGCCTTTACCTGCTAAGAAAAGGACAATAGAAAAAACACGGGGAAATGCGTGTGA 3781 GAATCCTGAAATATTAAAATACCCCCAATGAATAAGATAGAAGATGAGTCATTGCT 3841 ATAAAGCAGAACATCATTGTAACTCTAAATTTGAAATATTCAACTTGGCTTCGCAATTGC 3901 TCAGTCCCCGTTCTGTTTGCAATTGAAATATTCAACTTGGCTTCGCAATTGC 3961 ATTACATCTTTAGAAAATGTAATGTTGCAAAAAACCGAACGCTGTAGTTTAGAA 4021 AATCTCAGACACTGAATTGTATGCATTCTAAATTCTGGGTGTATTCTAACAGGAAGACT 4081 CTCAACATGTCCTGTTAGTGGGAAATATGAGAGTGAAGAACATTAAATGGCAACAAAT 4141 ATCCTTTTAAAGGCACCTAAATAGAGCATTAGACATTATCAATATAGATAGTGC 4201 TTGCCCAACTTCACAATTAAATTAGCTGTTGCCTTTGCATTATTAAATACTTAAGTG 4261 CTGGAGTTATAAAAATGAGCTAATCTACATCAGGCATGCTCTAGAAATCCCTGCA 4321 GCCTGAAAATAACAGCTGTCAACCAGAGATTGTGTAAGAACATTAAATTTAGAAAA 4381 TAAATGGTGAACATGCTCCTAAAAACATTATTGTGATGGGATAAGATGGTGTATTAG 4441 AAACCCAGGTATTAGGTAATTGTGGTGAATTAAAGGTACTGCTGTATCCATA 4501 TCAGTGGATCTGCTTTGATCAGTTCATCTAAATATAAGATACTGTCTCTTAC 4561 CGTTACATACAGCCAGGAAAGACAGCCCTAGTGGTGGGTACTAGAGTTGGAGGAACAAG 4621 TGAACCTGTGGTTTCCCTTGTGAAATGTTGACATTCTGACAGTCTGATTGGCCT 4681 TCTGTTCTCATGCTTGCTAACTCACTAGTGTCTCAAAGAGAGCCTGAATTAAATAGGT 4741 ATGGTCTAACACAGTTGAAATAACCTTGTAAGAACATATGAGAGAAAATCTAAAGCAAA 4801 AATTAAGCTGCCACCTAAGGGACATATGAATTATTACATCTTGTGATGCCCTTTCA 4861 TCAATATTGAGAGATTGCTAATGTGATCATCAGATTGCTAATCTGCCAGCATGTTCTA 4921 CCAGCATTTCAGATAATACAGAATATGGTTCTAGCAAAGTTGGTCTTTATTTC 4981 TTAGAATCACAGGAAAGACATATTGGTTGATAATAGGTTATTCTATTGGGGACTA 5041 ATAATTCTGATATATATTAGGATTCTTAAACACCACTCTAGGTAATGTTGCAATAG 5101 TATCTCACTGGAAATGAAAGACTATCAAGGTGTTCACTTGATAGTTAGAACCAAGGGTG 5161 AACAGTCTTGCTTTATTAAAAAAAGTCTAAIGTTCTATTGCTTTGATATTG 5221 CTTTGATTAACATCCTGGAAACCAACACATTGAATTTCAGTATTGAAACATAGTGA 5280 CCAAAGTAAAGAACCAAGTGGTATAATGCTTCT 5281 AGTAATTCTTTATATGTAATCAAGTCATAAAGAACCAAGTGGTATAATGCTTCT 5340	5340
5341	GGGGGCCATCCTTGCTGTTACACCCCTAACCTCCATCACAGGAAACATGACAGCTGCC G N M T A A L	5400
5401	TACAGGCAGCTCTGAAGAACCCCCCTATCAACACCAAGAGTCAGGCAGTGAAGGTGAGTC Q A A L K N P P I N T K S Q A V K	5460

Fig. 22 (continued; 3/5)

5461	GCAGACTACAACACAGTGATCTGCTGATATCTTATTCTTAGTAAAATCCTTGAGTGC	5520
5521	AAAAAAAAAATCAATATTTAACGTGTTGCTATCTTGACAAGAAGAGTTATAATGTAGT	5580
5581	TTGATAGGTAAAAATTCACGTAAAAAATAGCCCTATAATGTAGTTATGATAATGCTGC	5640
5641	ATGGTAAGATAACAGTAAGTCAACGATAGTGAATCATTTGTGTGTTTAGAGGAG	5700
5701	ACCACTCAGGCTGAATTGAGCAAAGGTTGAAAAATAAGTAAACCTTACAAAATAA	5760
5761	ACAGATTGTAATTGCTTTAAAGATTTTAAACCATACAAATACTAAATCTTATTA	5820
5821	TAGAAAGCTCAGACATATGAGAAGGTTAAAAGATAGTGGTTGGTCCCAGCACCCAG	5880
5881	AGATAACAGTTACTACTTGGGGCCTTGCTGTATTGTTACAGAGTCCCTTGT	5940
5941	TAAGAATGAATTTTAAAACGGGTTTTCAGCTATATGCAATGGTACATGAGCCTTCCT	6000
6001	TCCCCAATAAGTTAATAGCCTTTAACACTTGTATATGGATAAGCTCCAGTGTATACA	6060
6061	TAACTAATCTTTGTTATATTAGACTGACTTTTTCTATGTAAACCAGTGA	6120
6121	TCAATATTTTGGTAAATTAAATTGTTCTTGTGAGTAAATTGCTAGCAGTGAATTA	6180
6181	CTGGATCAAAGAATGCACTTTTTAAGGTTTGGTATGCAGTATTGCCAATTGCC	6240
6241	TTCAAGAACAGTTGTGCAACTACATTCTCGAGTCTTACTAATTCTAACCTATTTA	6300
6301	CGTATTATTTAAAATGATGCCATAGCATCAACCCGTTGTCATAGCTATTACAT	6360
6361	CCTAGGAGCTTCAAGAATCTCAATTGAATAGTAGTAAGTAAATAACTTAGTAAATGCATA	6420
6421	ATAATTATCTAGGTAACATAATTTTTATTGGGAAAATTCTTGGTTTACAAGTTG	6480
6481	TAAAGATTGTCGTTGAAATTTCATTTTACCGTGGATGCAAAGATATTCTAAATCTG	6540
6541	GTAATTGCAGTCTTAAACAAAGATAACAGTAGGTGGTAGAAACATTCTGAAATCCT	6600
6601	GACCAGTAGGAATGCTGGAGGTACTTGTGTTGAATGGAAGGGAGAACGAAATTGTTG	6660
6661	AAAAGGTCAAGTTAAGTGTTCCTTGCTTGGCCGGATGGTAAGAAAATAACTGTTTG	6720
6721	AAGCAGGCTTGCACAAAGAAAAAGATCATTATTAAATGAACATCACTATATTCAATAC	6780
6781	TACAGTCATTCAATAAAATTACAGTCATTCTTTAAGACAGCTGGTTATTAAAA	6840
6841	TTTTAAATAAAAAGTTTAAGAAAAAATTACTCTGAAGGATAATTCAAGGTGAAAC	6900
6901	TGCAAATCTGCCTCCTGTTGGAAATTTTTTTTTTTTGAGACG	6960
6961	GAGTCTCACTCTATCACCCAGGTTGGAGTGCAGTGGTCAATCTCAACTCACTGCACCC	7020
7021	CCGCCTCCGGGTTAACGCAATCCCTGCTCAGCCTCCGAGTAGCTGGATCACAGG	7080
7081	CACACACCACATGCCTGGATAATTCTGTATTAGAAGAAAACAGGGTTTACCAATT	7140
7141	TTGGCCAGGTGGTCTGAACTCCTGACCTCAGGTGATCTGCCATCTGGCCTCCAAA	7200
7201	GTGCTGGGATTACAGCTGTGGGCCACCACACCGCGTTTGTGGATTTTTTTT	7260
7261	TAAGATCAAGACATAATTAAATGTTTTAATAAAATTGTTAAATTATCACATTGATC	7320
7321	TGTTAGCAAATCCTCTCAGCTGCCTCAATTATGTTAATAGTCTGTCAGTTCTTAC	7380
7381	CACCTCCACTGCTACTATGCTTACACATCCAGCCTGTATTATTGCAATTGCTCCTAAT	7440
7441	TGCTCTCCCTGCTTACCTTACCTTACTCCCACAGCTTATTCTGTAACATAGATG	7500
7501	CCAAAGCAATCCTGTTAAATGTGAGTCAGATTATGGCACTGCTCTAAACCTCCAAT	7560
7561	GTCTTCTCATTCTCTCAGTAAAGCCAAACTCCTTACAATGCCTGTAGGCCTTACACGA	7620
7621	TCTGTCCTCCCATAACCTCTGACTTACTCACGTGCTTCTCCCACCAATCCACTCCAAC	7680
7681	CACATTGGGTTTTCTGTTGGAACACACTGAACACACACTAATGCACTGTTCTT	7740
7741	TCCCTGTCGAAACACTTCTCAGTTATCCAAGCCTTCTTCACGTCTCAGGTCC	7800
7801	TTACTCAAATGTCACATTCAAGTGTAGACTTCTGAAATTCTAAACCTCCTACACAG	7860
7861	ATATGTCTAAATGTTCTGTTATTGACCCACCAGGACCGGGCAGGCAGCATTGTCTT	7920
	D R A G S I V L	
7921	GAAGGTGCTCATCTCTTTAAAGCTAATGATATAGAAAAGGCAGTCAATCTGGACAA	7980
	K V L I S F K A N D I E K A V Q S L D K	
7981	GAATGGTGGATCTCTAATGAAGTATATTATAAGGATTGAGAGGCCGTGACAA	8040
	N G V D L L M K Y I Y K G F E S P S D N	
8041	TAGCAGTGCTATGTTACTGCAATGGCATGAAAGGTAAAGTTATGAATTATAAATCTATAT	8100
	S S A M L L Q W H E K	

Fig. 22 (continued; 4/5)

8101	GACTGGTTCTTACAATAGGAATGACAATGACAACCTCTCACCTAAATAACCATT	3160
8161	TGATTTGTGACATTGGTATTACAAATAAATGCATGAAAAGGATAGTCATATT	3220
8221	ATGTTTACTAGCCTGGTCTAACAGATTCTGATTCAACACTGTGTTTTCAACAT	8280
8281	GATTATTAGTAATTAAACATAATCTGAACTCTGAATTAAATCAAAACTTTGAAAAGAA	8340
8341	AATAAGCAATACAAATCAAGAATTCTTCACAGTGACCAAAAGGTGAAAACACAAAGG	8400
8401	ATCGAATATGATTCAACCA	8419
8420	TTAAAAGGAATGACATTCTGACACATGCTATAACATTAAACCTTGAAAACATACCAA	8479
8480	GTGAAATGAGCCAAACACAAAAGAACTAATATTATAATTACTTATGAAATAATC	8539
8540	TAGGATAGGCAACACAAAGGGACAGAAAGTCCTTAGAGGTACTAGGAAGTAGGGAAAG	8599
8600	CAAGGAATAGGGAGTTAGTGTCTAACAGGTACAGAGTTCCTCCTGGAGTGGAAAAAG	8659
8660	TTTGAAACAGATAGTGGTGTGGCTACAGTACATTGTGAATATAATTATGCCAATGG	8719
8720	ATTTTACACTTAAAGATGGTAAAATGCCAATTGGTGTAGATAATTACAACTTTT	8779
8780	TAAAGAATTAGGAGTTGGAGGATCAAGAATTCTAAATCATGTTTCTATTTCATGT	8839
8840	GTATATTTCGAATGTAAGTAGATGCTGGTACATCATCTGTCAAAAGAGTATAAGTGATT	8899
8900	TTGAGCTTGGTAAAAAACTGGATAACATGTAAATAGAACCAAGTCATAAAATATTGAG	8959
8960	TGTTGAAAGTGTATCTGAGTGAAAACACAAACATAAGAAAAAGCACATAGTAAACAAAT	9019
9020	AGTTCCCCCTTTACTCTAAATGCACCAATTGGTAGTAATTATGACCCCTATT	9079
9080	CATGGAACACTTCTGTTGCCAGGTACCATACTATTAAATGTTTATTTAACCTTACAAC	9139
9140	AACCTGTGGAACTTAAATATCTTATCATCTCAATTACAGATGAAAGCTAGCT	9199
9200	TTAAAACCCAAGCCAGCGTAGTTCTAGCATAGCCTCAAGATTGCACTGAACTTGATTAC	9259
9260	TTATTATATTCCACATATTCTCAAAGGACTTTATAAAATTAAACTCATTTAACCTCAT	9319
9320	AAAAATGGAGGGAAATGCTTGCTATTATTCCCTTTGTCACTGAGGAAACTGAGGCATG	9379
9380	TGTGAAGTCTTCATTTCTCAAATGTCAGTCACCAGTTTACCAATCTCGAAGTATT	9439
9440	TCTGAAATCTATCTGTTCAAGCGTATCTAATGCAGCTGTCACAGCATCTCCCAGTCT	9499
9500	GTTGCCATAGCTTCTGACTGGTTCCAGTTAACAGTTTGCCTCCTTCAAATCTGTC	9559
9560	TCCACCCAGCCATCAAAATGATATCTTAAATCAAAATTGCCCTGTCAGTCACCTGCA	9619
9620	GGGATAAAAGTCAAAGTCCCAGTCTAGCTCATCTCCATGTCATTCTCCCTCAGGC	9679
9680	TATAGCAATGCCAGCCTTTCTGAATGCACCATATTGTTCACACCTCCATACATTG	9739
9740	CTCATGATTTCTGGTGTAGCCTGTACCTACTCATTTAAATGTTGTCATTCTCC	9799
9800	ATGAAGCCTTAGCTGAAACATTCTCTATACTGTTAATCTGGGTATAAGCCTCTCC	9859
9860	TGCTTAAATAGCACCTGCAGCACAACTCTATTACATTAGATAAAATTACCTGTT	9919
9920	TATATGTCCTGCTCCTCATGCTAGACCAAGAAAATGCTGATTGTTCACTTTGTATCCC	9979
9980	CAGCATCTAGCACAGTACTCAGTACACAAAGGTATTCCATAAAATTGTTAACAGAAA	10039
10040	GAAACCAAGCTAGATTCTAATACTGATCATACTCTCATTTCAAATTAGAGTC	10099
10100	AGAGTTAAAGTTCTAAGTCTTAGCTATTAAACAAATACCTTCTTCTTGGAGAAAAA	10159
10160	AAATCTGACAAAGGCTGACTAACATGAAAGTGGAGTTGGATGGTGTACCCAGTTGAAT	10219
10220	TTTCTCTGACTATGTGGTGAGAATGCGAAATGTCACCTGTTGAGCAGGA	10279
10280	ACACTATGCTGCAGATTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	10339
10340	TCTGTCGCCAGGCTGGAGTGCAGTGGCGCAATCTCGCTACTGCAAGCTCCGCCCT	10399
10400	GGGTTACACCATGTCCTGCCCTAGCCTCCGAGTAGCTGGACTACAGGCACCCGCA	10459
10460	CCACGCCGGCTAATTCTGTTAGTAGAGACGGGGTTCACCATGTTAGCCAGG	10519
10520	ATGGTCTTGATCTCTGACCTCGTGATCCGCCGGCTCGGCCCTCCAAAGTGCTGGGATT	10579
10580	ACAGGGCTGAGCCACCGCGCCGGCTATGTCAGATTAAACATTATTAGAAT	10639
10640	TAATGTTAAATGTAACACTAGTATCTCACTAGAACATGTAACCTCATGAGGGCAGGGACT	10699
10700	TTCAAGGTTTGTATTACTGTAACCTCAGTGCAAGAACAGTACCTGGTGCATAATTG	10759
10760	GTGCTCAAGAATTATTGTTAACATAAAATTCAAGGGCTATAGCAGTGCCCATTC	10819
10820	CTTCTTAAGAAAAATGTTACCAAATATGAGAAATTGACCTTTATTCTGTCAACAA	10879
10880	TTTACATCCTGGTTGTTAGGCACCTGCTGGAGGAGTAGGGTCCATTGTCGTG A L A A G G V G S I V R V	10939
10940	TCTTGACTGCAAGAAAAACTGTGAGTCTGGCAGGAAGTGGATTATCTGCCCTGGGAGTG L T A R K T V *	10999

Fig. 22 (continued; 5/5)

11000	GGAATTGCTGGTACAAAGACCAAAAACAACCAAATGCCACCGCTGCCCTGTGGGTAGCATC	11059
11060	TGTTTCTCTCAGCTTGCCCTCTGCTTTCTATATCTGTAAAGAAAAAATTACATATC	11119
11120	AGTGTGCCTTAATGAAAATTGGGATAATATAGAAGAAATTGTGTTAAAATAGAAGTGT	11179
11180	TCATCCTTCAAAACCATTCACTGATGTTATACCAATCTGTATATAGTATAATTACA	11239
11240	TTCAAGTTAATTGTGCAACTTTAACCCCTGTTGGCTGGTTTTGTTCTGTTGTT	11299
11300	TGTATTATTTTAACTAATACTGAGAGATTGGTCAGAATTGAGGCCAGTTCTTAGCT	11359
11360	CATGCTAGTCAGGGAAATGATATTATAAAAATATGAGAGACTGGCAGCTATTAACAT	11419
11420	TGCAAAACTGGACCATATTCCCTATTAATAAGCAAAATATGTTTTGGAATAAGTGG	11479
11480	TGGGTGAATACCACTGCTAAGTTAGCTTCTCTCAGCATCCAATAATCATGGCCCTCAATTATT	11539
11540	TGTGGTTAAGTATGCTACTTTCTCTCAGCATCCAATAATCATGGCCCTCAATTATT	11599
11600	TGTGGTCACCCAGGGTTCAGAGCAAGAAGTCTGCTTATACAAATGTATCCATAAAATA	11659
11660	TCAGAGCTTGGGATGAACATCAAACCTTTGTTCCACTAATATGGCTCTGTTGGAA	11719
11720	AAAATGCAAATCAGAAAGAATGATTGAGAAAGAAAAGACTATGGTGTAAATTAA	11779
11780	ACTCTGGGCAGCCTCTGAATGAAATGCTACTTTCTTAGAAATATAATAGCTGCCCTAGA	11839
11840	CATTATGAGGTATACAACTAGTATTAAAGATACCATTAAATATGCCCGTAAAGTCTTC	11899
11900	AGTGTCTTCAGGGTAGTTGGGATCTAAAAGATTGGTCAGATCCAACAAACACACA	11959
11960	TTCTGTGTTTAGCTCAGTGTCTAAAAAAAGAAACTGCCACACAGCAAAATTGTT	12019
12020	TACTTGTTGGACAAACCAATCAGTTCTCAAAAATGACCGGTGCTTATAAAAAGTTAT	12079
12080	AAATATCGAGTAGCTCTAAACAAACACACCTGACCAAGAGGGAAAGTGGCTTGCTTAG	12139
12140	TATTACATTGGATGCCAGTTGTAATCACTGACTTATGTGCAAACACTGGTGCAAGAAATT	12199
12200	CTATAAAACTCTTGCTGTTTGATACCTGCTTTGTTCTATTGTTGTTGTAA	12259
12260	AAATGATAAAACTTCAGAAAATAAAATGTCAGTGTGAATAATTATTTCTGACAC	12319
12320	TTAACAAATTATGAATGATGGTTAATTAGAGGGAAAGGTTCTGCTTCTACCCACCAAG	12379
12380	TACTGTACTCTAACAGAACAGTTGGTAGGGTTTTATAAGACTATAGATATAAGA	12439
12440	TGATAGAGAAGAGAGTCATGAATGATGTCAGAGCACTACTGAAGCCTTGGAGTGATTCC	12499
12500	ATAGCCTCTGGATGGCAGCTGAATACCTATATGAGTACACTGCCAAAGACCTAGAC	12559
12560	TAGAAAGTGCAGAAAGTAGCTTAGCAGCTGCAGTCATTCACTCCAGCCTCCAAAATTCTCT	12619

Fig. 23 (1/6)

1 - GATCCCTCTCCAGGTGGAAG - 60 / \\
 61 - CTCCTTCATACCAAAGTTAAAGGCCCTGGGATACGAGTAACCTTGACGACTATGAGG - 120 |
 121 - AAGAAGAAATCCGGTCTCATCAATGAGAAGTGTGGCAAGGAGTTCTGAGTTTAGG - 180 |
 181 - GGCGATGCCGTGCCCCCATGGGTTCTTTCTTTCTTTCTTTCTGGTCGGGGGGG - 240 |
 241 - TGGGAGGGTGGATTGAACAGCCAGAGGGCCCCAGAGTTCCTGCATCTAATTCAACCC - 300 |
 301 - CACCCCACCCCTCAGGGTTAGGGGGAGCAGGAAGCCCAGATAATCAGAGGGACAGAAACA - 360 |
 361 - CCAGCTGCTCCCCATCCCCCTCACCCCTCACCCTCCTGCCCTCTCCACTTCCCTCCTC - 420 |
 421 - TTTCCCCACAGCCCCCAGCCCTCAGCCCTCCAGCCCCTGCCTGTTAACGA - 480 |
 481 - GTTTCTCAACTCCAGTCAGACCAGGTCTGCTGGTGTATCCAGGGACAGGGTATGAAAG - 540 |
 541 - AGGGGCTCACGCTTAACCTCAGCCCCACCCCACCCCCATCCACCCAACCACAGGCC - 600 |
 Human cAMP-dependent protein kinase
 catalytic subunit alpha
 Accession number X07767 (until *)
 - follow arrow until line that
 begins 1561 -

601 - CACTTGCTAAGGGCAAATGAACGAAGCGCAACCTTCCCTCGAGTAATCCTGCCTGGG - 660 |
 661 - AAGGAGAGATTTAGTGACATGTTAGTCCACCAGTGCCTCCCTCCCTACTCCC - 720 |
 721 - AACAAATTAAAATCTTATTAAGTCCACCAGTGCCTCCCTCCCTACTCCC - 780 |
 781 - ACCCCTCCCATGTCCCCCATTCCTCAAATCCATTAAAGAGAACAGACTGACTTTGG - 840 |
 841 - AAAGGGAGGCCTGGGTTGAACCTCCCCGCTGCTAATCTCCCTGGGCCCTCCCCGG - 900 |
 901 - GGAATCCCTCTGCCAATCTGCGAGGGTCTAGGCCCTTAGGAAGCCTCGCTCTT - 960 |
 961 - TTTCCCCAACAGACCTGTCTCACCTTGGGCTTGAAGGCCAGACAAAGCAGCTGCC - 1020 |
 1021 - TCTCCCTGCAAAGAGGAGTCATCCCCAAAAAGACAGAGGGGGAGCCCAAGCCAACT - 1080 |
 1081 - CTTCCTCCAGCAGCGTTCCCCCAACTCCTTAATTCTCCGCTAGATTTAAC - 1140 |
 1141 - GTCCAGCCTCCCTCAGCTGAGTGGGAGGGCATTGCAAAAGGGAACAGAAGAGGCC - 1200 |
 1201 - AAGTCCCCCAAGCACGGCCGGGGTCAAGGCTAGAGCTGCTGGGAGGGCTGCCTG - 1260 |
 1261 - TTTTACTCACCCACCAGCTTCCGCCTCCCCATCCTGGCGCCCTCCTCAGCTTAGCT - 1320 |
 1321 - GTCAGCTGTCATCACCTCTCCCCACTTCTCATTTGTCTTCTCTCGTAATAGA - 1380 |
 1381 - AAAGTGGGAGCCGCTGGGAGCCACCCATTCACTCCCGTATTCCCCCTCTCATAACT - 1440 |
 1441 - TCTCCCCATCCCAGGAGGTCTCAGGCTGGGTGGGCCCCGGTGGTGCAGGGGC - 1500 |
 1501 - GATTCAACCTGTGCTGCGAAGGACGAGACTTCCCTTGAACAGTGTGCTGGTAAAC - 1560 |
 1561 - ATATTGAAAATATTACCAATAAGTTGT*TAAAAAAAAGTGTGCTGGTGTCTC - 1620 |
 1621 - GACTTCGATCACCCACCCACACACCCCCAGGGGTTGGAAAGGGATTGGACCCCAGC - 1680 |
 1681 - GTGCAGGCCGATCAGGTCTGGCTGAAGTCCTGTAACCAGGGTTAGCTGAAATTCCG - 1740 |
 1741 - GCACTCCTTCGGCCCGCAGGAGAACGAGCTCAAACCTGCCCTTGACCCAGATTGG - 1800 |
 1801 - GGTCCCCAAATCTGCGCGCGCCCCCTGGCGTCCAGCCGGGACCGAGAGGGCGCTCTA - 1860 |
 1861 - GGGAGGGCTGGGCTGGCGCGCCAGGAGGCCAGCGGGCGGGGGCGGCCCTGGCAGG - 1920 |
 1921 - GGGAGTAGAAGGGGAGAGGGTGCAGGCCCTTCCGCATCCTCAGGCCGGGCCAGG - 1980 |
 1981 - CGCGCCTGAGGGACGCCGGGGCGGCCAGCAGCAGGAGGGTCCCCCAGCACCTCTGAGCG - 2040 |
 2041 - CGGCAGCCCCGGCCCGCGGGCGAGTCCCGTAAAGTGCCTCCGAGAGCGGAGCGC - 2100 |
 2101 - GCTGGAGAGGCGTGGAGAGGGGGCTGGCGCCGGGACGTCTGGTCCCGGCCAATG - 2160 |
 2161 - GCTGGAGGGCGGCCAGCGCCGCCCTGCCGCCTGCCGCCCTCTCCCCCTCCCCCGG - 2220 |
 2221 - CACTCCCCCTCCCCCTCCCCCGCCGCCGCTTCCCCCGCCCCCGGCCACTCC - 2280 |
 2281 - GCGGCGCCTCTTAAAGCGCGCGGGAGTTGTAAGGGGGGCCGGAGCGAGCGGAGTG - 2340 |
 2341 - AGCGAGAGCGCAGGGTAAAGGGGGCGGGGGGGGGGGCTCCACCTTAAAGCGGGC - 2400 |
 2401 - GCGTGGGGGTGGGAGGGAGGAAGGCGGGCGGGAGGGAGGGAGGGAGGGAAAGGG - 2460 |
 2461 - GGGCGGGAGTGTCCCGGGCGCAGGGCGCGTGCAGGCGGGCGGGGGAGGGGCC - 2520 |
 2521 - GGCGCGCCCGCGCTCCCCCTCTCCCCCGCAGCACCCGGCCCGCGGCCAGCAGAA - 2580 |
 2581 - GCGGGTCTGTGTGCGTGCAGTGAAGTGTGCTATTTTCTCTCTCTCTCTCTT - 2640 |
 2641 - TCTTTCTCTCTACTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTT - 2700 |
 2701 - TTTTTTTTGTGCAAAGAACAGCAGCGCCGCCGCGTCCGCGAGGGCGCTGCCTCC - 2760 |
 2761 - GGGGGGGAGGCAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGCCGGGGAGGGGCC - 2820 |

Fig. 23 (continued; 2/6)

2821 - CGCGCTGGGAGGGAGGCAGCGCAGCGCACGGTGCAGCCGGCCGGGGAGGCATGGCGGG - 2880
- M A G

2881 - CCCCCGGCCCTACCCCCGCCGGAGACGGCGGCCGGCCACCACGGCGGCCCGCCCTCG - 2940
- P P A L P P E T A A A A T T A A A A S

2941 - TCGTCCGCCGCTTCCCCGCACTACCAAGAGTGGATCCTGGACACCATCGACTCGCTGCGC - 3000
- S S A A S P H Y Q E W I L D T I D S L R

3001 - TCGCGCAAGGCCGGCCGGACCTGGAGCGCATCTGCCGGATGGTGCGGCCGGCACGGC - 3060
- S R K A R P D L E R I C R M V R R R H G

3061 - CCGGAGCCGGAGCGCACGCCGCCGAGCTCGAGAAACTGATCCAGCAGCGGCCGTGCTC - 3120
- P E P E R T R A E L E K L I Q Q R A V L

3121 - CGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCCGGCGCGTCCAGGCCGCCGG - 3180
- R V S Y K G S I S Y R N A A R V Q P P R

3181 - CGCGGAGCCACCCGCCGGCCCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC - 3240
- R G A T P P A P P R A P R G A P A A A A

3241 - GCCGCCGCCGCCGCCGCCACGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC - 3300
- A A A P P P T P A P P P P P A P V A A A

3301 - GCCCCGGCCCCGGCGCCGCCGCCGCCGCCGCCGCCACAGCGCCCCCTGCCCTGGC - 3360
- A P A R A P R A A A A A A T A P P S P G

3361 - CCCGCGCAGCCGGCCCCCGCGCGCAGCGGGCCGCCGCCCTGGCCGCCGCCGCCGCG - 3420
- P A Q P G P R A Q R A A P L A A P P P A

3421 - CCAGCCGCTCCCCGGCGGTGGCGCCCCGGCGCCGCCGCCGCCGCCGCCGCCGCC - 3480
- P A A P P A V A P P A G P R R A P P P A

3481 - GTCGCCGCCGGGAGCCGCCGCTGCCGCCGCCACAGCCGCCGGCGCCACAGCAG - 3540
- V A A R E P P L P P P P Q P P A P P Q Q

3541 - CAGCAGCCGCCGCCGCCAGCCACAGCCGCCGGAGGGGGCGCGGTGCGGGCCGGC - 3600
- Q Q P P P Q P Q P P P E G G A V R A G

3601 - GGCGCGGCCGGCCCCGTGAGCCTGCCGGAACTCGTGCCTACCTCGGGGCCAGCGGCCGGC - 3660
- G A A R P V S L R E V V R Y L G G S G G

3661 - GCCGGCGGTGCCATAACCGCGGCCGCGTGCAGGGCTGCTGGAGGAGGAGGCCGGCT - 3720
- A G G R L T R G R V Q G L L E E E A A A

3721 - CGAGGCCGTCTGGAGCGCACCCGTCTGGAGCGCTTGCCTGCCGCCGGGACAGGCC - 3780
- R G R L E R T R L G A L A L P R G D R P

3781 - GGACGGCGCCGCCGGCCAGCGCCGCCGGCTCGCAGCAAGGTGAGCGGCCGGGG - 3840
- G R A P P A A S A R P S R S K

3841 - AGCGGGGGCGCCGCCGGCGTGGCAGGTGCAGGGGAAGTTGGTGGCGGGGGCGCGAGTCCC - 3900

3901 - GGGAGGAACTGGGTGGCGGGTGGCTGGGGCTTGCCTGCCGGCTCGGTGCG - 3960

Fig. 23 (continued; 3/6)

3961 - TGGTACCTTGCAAGTGATTGAACTCCCGAGCCTCAGTTCTCCGCTGTAAACGCG - 4020
 4021 - GTTTATAAACAGTAGCGACCCCTGGGGTTGTTGAGCGAGTTAGTAAGATTTGGTTGTC - 4080
 4081 - GAGGGCTTACTTAACACAGAGCCTGGCACGGAGTGAATCGTAAAGATTTAGTCCTGATT - 4140
 4141 - GTTCTTAAAGGTGGAATCGTTCTCCCTCCCCACGCCCGACGCCACAGTCAGGGTCTG - 4200

 4201 - GGATTAGAACAGCTACTAATTTGCATGCTCTCCTCGGCTCCAGAGAGGTGGAGAAG - 4260
 - R G G E E

 4261 - AGCGAGTACTTGAGAAAGAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATG - 4320
 - R V L E K E E E D D D E D E D E D D

 4321 - ATGTGTCAGAGGGCTCTGAAGTCCCCGAGAGTGACCGTCTGCAGGTGCCAGCACCACC - 4380
 - V S E G S E V P E S D R P A G A Q H H Q

 4381 - AGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGGAGAGGGTCAAGGAGTGGACCCCT - 4440
 - L N G E R G P Q S A K E R V K E W T P C

 4441 - GCGGACCGCACCGGCCAGGATGAAGGGCGGGGCCAGCCCCGGCAGCGGCACCCGCC - 4500
 - G P H Q G Q D E G R G P A P G S G T R Q

 1 - AGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGAAACAGGTAAAGGATCCCTCTGGGT - 60
 - V F S M A A M N K E G G T

 61 - GGGGAAGAGTGCTAGGTGGAGAGGAACAGGTAAAGGATCCCTCTGGGT - 120

 121 - TTTCCCTCCCAGCTTCTGTTGCCACCGGGCAGACTCCCCGTCCCCGTGCCTTGCCC - 180
 - A S V A T G P D S P S P V P L P

 181 - CCAGGCAAACCAGCCCTACCTGGGGCGACGGGACCCCTTGGCTGTCCGTAAGTTGGG - 240
 - P G K P A L P G A D G T P F G C P

 241 - GTATTGGAGACATGGGGTGCTGCTCAGGTGTGGTACAGCCAGAGAGACATCCGTGTT - 300

 301 - CACTGGGTCTGTTGTTGATGCAGTCCCAGCGCAAAGAGAAGCCATCTGATCCGT - 360
 - P G R K E K P S D P V

 361 - CGAGTGGACCGTGATGGATGTCGTCGAATATTTACTGAGGCTGGATTCCGGAGCAGGC - 420
 - E W T V M D V V E Y F T E A G F P E Q A

 421 - GACAGCTTCCAAGAGCAGGTGAGTTCCAGCCCAGGACTACACACTGACAGACACAGAG - 480
 - T A F Q E Q

 481 - GGCTCCCTGGATGTGCCCTGATCCGGTTCTGTTCTGTCCCACCCAGGAAATT - 540
 - E I

 541 - GATGGCAAATCTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGCCTGTCCATCCGC - 600
 - D G K S L L M Q R T D V L T G L S I R

 601 - CTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAGGTGCTTCAGCAAGGCCACTT - 660
 - L G P A L K I Y E H H I K V L Q Q G H F

Fig. 23 (continued; 4/6)

661 - GAGGATGATGACCCCGATGGCTTCTAGGCTGAGGCCAGCCTCACCCCTGCCAGCC - 720
 - E D D D P D G F L G *

721 - CATTCCGGCCCCATCTCACCAAGATCCCCAGAGTCAGGAGCTGGACGGGACACCC - 780
 781 - TCAGCCCTCATAACAGATTCCAAGGAGAGGGCACCCCTTGTCTTATCTTGCCCTTG - 840
 841 - TGTCTGTCTCACACACATCTGCTCTCAGCACGTCGGTGGGAGGGATTGCTCCTTA - 900
 901 - AACCCCAGGGCTGACCCCTCCCCACCCAGTCAGGACATTAGGAAAAAAATGAA - 960
 961 - ATGTGGGGGCTCTCATCTCCCCAAGATCCTCTTCCGTCAGCCAGATGTTCTGTAT - 1020
 1021 - AAATGTTGGATCTGCCTGTTATTTGGTGGGTGGCTTCCCTCCCTACCACCC - 1080
 1081 - ATGCCCCCCTCTCAGCTCTGCCCTGGCCTCAGGCCCTAGGGACTAGCTGGGTGGG - 1140
 1141 - TTCTCGGGCCTTTCTCTCCCTTTCTGTGATTGTCGCTCAGCTGGCTG - 1200
 1201 - TATTGCTTTAATATTGACCCGAAGGTTTTAAATAAAATTAAATAAAAGAGG - 1260
 1261 - GAAAAAAAAGCCACGGAGTCATTTATGAATGGGTGGGAGAGGGCACTAAAGAGCCT - 1320
 1321 - CCTAAGAGAGCCTCAGGTAGGACAGAATTGTTGGGAGGGAGAAAACAGAAACAATG - 1380
 1381 - AATTATAGCTGCCTCACAGCCATGTATAACAATAATTGCTCCAGGAAGGTGGGAATATT - 1440
 1441 - GCTTTTTTCTCTGTAACTCACCGTGTCCAGAACAGAGCTAGGCACACAGC - 1500
 1501 - AGGTGCTCAATTGTTCTAGACAGGTTCTTACCCAGGCTGGAGTG - 1560
 1561 - CAGTGGTGCTATCATAGCTCATTGTAGCCTCAAACCTCTGGCTGAAGTGTACCTCCCAC - 1620
 1621 - CTCAGCCTCTGAGTAGCTGGACTACAGGTGCACTCTGCCATGCCGGCTAACCTTAA - 1680
 1681 - AAATTTTGCCGGCACAGTGGCTCATGCCGTAACTCCAGCACTTGGGAGGGCGAGG - 1740
 1741 - TGGGTGGATCATGAGGTCAAGGATCAGCCTGCCAAGATGATGAAACCCCTGTC - 1800
 1801 - TCTACTAAAATATAAAAAAAATTAGCTGGCGTGGTGGTGGCTGTAATCCTAGC - 1860
 1861 - TATTAGGAGGCTGAGGCAGAGGATTGCTTACACCTGGGAGGCGGAGGGTGAGCC - 1920
 1921 - AAGATCGTGCCTACTGCACCTCAGCTGGGTGACAAGTGAAGACTCTGTCTCAAAAAAA - 1980
 1981 - TCTTGTGTGTGGAGATGAGGGTATGCACCTTGTGGCCAGGTTGGCCTCGAAGTC - 2040
 2041 - CCAGCCAAGCAATTCTGCCTGGGATTACAAGCGTGAGCCACATGCCCTCAAATAT - 2100
 2101 - TGTTGAATGGCTAGCAGTTAACGTTGGGTTATAAGCATTCCTCAACTGTCTCCCA - 2160
 2161 - AGTCCCCATAAGACAAAAACTCATAAATCCACCTACAGAAGAGGCAGCTGGCCGG - 2220
 2221 - CACAGAGATGCTGTCTGCCCGGGTCACACAGGGTGGCATCTGACACCCCTGTGAGTC - 2280
 2281 - TTCACTCAGAGTCTTAAATATAATTAGCGTATTGACATAATGTACATTAAAAGTATA - 2340
 2341 - AACCTGTCACTTGTACTGCAAAGAATCCACTACAAATATTGGGCAGGGATCTGT - 2400
 2401 - TCTTGGACCATAGTAGTGTCTCCAGACCTCATGGCTCTTCACTAAAACAACAGAAAAT - 2460
 2461 - TCCTTCTGGGCATCAGATGAGACCATGAGATAGAAGATTCCAAGTGAAGATTGT - 2520
 2521 - CAAGACAGAGTCTGCTCTGCACTCAGGCTAGAGTGTACTGGTGAATCATAACTGTGG - 2580
 2581 - TGACAGCCTCGAACCTTGGTACAAGTGATTCTCATGCCCTCAGACAACACCCAACTAAT - 2640
 2641 - ATTGTTGGTTTGTATAGACAGGGCTTGCTATGTGGCTTAGGCTGGTCTTGAACCTCTG - 2700
 2701 - GCCTCAAGCAGTCCTCCCGCTTCAGCCTCCTAAAGTGTCAAGGATTACAGACATGAGCCAC - 2760
 2761 - CAAGTCCAGCCTGAAGATTAAATTTAAAGAAAAAGAGGTGGGACTTGGCAACATGGGCCCCATC - 2820
 2821 - TCCAAAGCTCTACTAAGTCTAACGTTCAAGTAGTCCTACTAACGTTCTAACGGCAGTTCTCAACT - 2880
 2881 - CATTAGAGTTTTTGTAAAGAAAAAGAGGTGGGACTTGGGAGACCAACTGGCAACATGGGCCCCATC - 2940
 2941 - ACGGGAGGATCGCTTGAGTCCAGGAGTTGAGACCAACTGGCAACATGGGCCCCATC - 3000
 3001 - TCTAAAAATTAAATTTAAAGAAAAAGAGGTGGGACTTGGGAGACACGT - 3060
 3061 - CTGGGGCCTGGCGCCTCATCCATACCTGTGGGGTTGAGGGGTTGGAGACACGT - 3120
 3121 - TTAGAGACCCCTCCACTCTAGGAATCCACCTCGAGAGATAAGGTCCCGGCCAGCCAC - 3180
 3181 - ACCCCCAGGACACGGCCAGAGGCCACCTCCCTAGGCGGGTCCCTCCCCACGCCAGGTTTC - 3240
 3241 - CTGGAGCGCGTGCAGCGTGTGCAAGGGTAGGGGGCCAGGCGCGGACTGGAGAGG - 3300
 3301 - CGCGCCCTCCCGCTGTGAAATTCAAAGAGGCAGGCCAGGGCCAGTCGGAGGCTCCCGGGCGGGTCGAACCC - 3360
 3361 - GCTCCGGTGGAGAGGTCAAGGCAGGGCCAGTCGGAGGCTCCCGGGCGGGTCGAACCC - 3420
 3421 - GCGGCCAACCTGAGCAGCAGCGGAAGCTTAAAGAGGCTCAGGTTCCGCCCGGCCCTA - 3480
 3481 - CCATGGCTACAGAGCAGTGGTCAGGGGTGCGTCCCCCTGGACCTGGAGAAACACCGC - 3540
 3541 - CTCCAGACGCCCTGGAACCTGGACGCCGCCGTGCGGAGACCCCTCAGGTCACGCC - 3600
 3601 - CTGGCAGGCCCTGGAACCCATCTGAGCCGGATCCTGAAGATGCCAGGGCGGCTGGCTG - 3660
 3661 - AGGCCCGGGCTCCACGTCTCCCCAACCTCTGGTCCCCCGGCCAGCACCTC - 3720

Fig. 23 (continued; 5/6)

3721 -	CCCGCCTATCCCTGGACACTTGTTCAGCCCCATCACCAACAGCTGCGTACCTACTGA	-	3780
3781 -	AGAAGGCAGATGATTCCAGAGCTACTTGCTCTACAGGTGATGCTGGACAGGGTCCCAGG	-	3840
3841 -	TCCCCATGGGTAAAGGAGACTTGGAGGGGAGGGACAGGATGGGTACACACACCAGGGTC	-	3900
3901 -	GCAAAATTACAAGCGCTAGGAGCCAGAGGGAGACACTGGAAAGACTAGCATATTAGAAT	-	3960
3961 -	CCAGTTAACAGAGAATGAGGAAGACTGTAGAATTGGGGTAGGGGATGGCTATTACTG	-	4020
4021 -	TCGTGGCAGGGTGGGCTGGGGTTGTCAAGTCTTAGGACTTTCTCCAGTTTAAG	-	4080
4081 -	TGCTGTCTTACATTTGAGCCCTGTGCTGGCTAAACAAGACCCACCTGAGCCAACTTGG	-	4140
4141 -	CCTGCAGGACATCAGTTGAGACTCCAAAGGATAATGTGATTCCCAGACCAGGTTCCCT	-	4200
4201 -	GTGACTCTCAATTTCAGTGTCCATTGAAATTCTTAGGAGGCTGGGTTGGGTTGTTGC	-	4260
4261 -	GTGTTGTTTTGAGATGGAGTCTCACTCTGCGCCAGGCTGGAGTGCAGTGGTGAAT	-	4320
4321 -	CTCAGCTCACTGCAACCTCCGCCCTCCGGATTGAAGCAATTCTCTGCCTCAGCCTCCGA	-	4380
4381 -	GTAGCTGGGATTACAGGCCCAACATGTGTTGCCCGCTAATTTCCTTTCTT	-	4440
4441 -	AGTAGAGACAGAGTTCAACCCTTGGCCAGACTGGTCTTGAGCTCTGACCTCATGATC	-	4500
4501 -	CACCCGCCTTGGCTCCCAAAGTGGTGAATTACAGACGTGAGCCACCGCGCTACCCGA	-	4560
4561 -	GGCTGGGTTTTTGTGTTGTTGTTATGTGTTTTGAAATGGAGTCTGCTCT	-	4620
4621 -	GTCACCTAGGCTGGAGTGCAGTGGCGAACACTGCAACTCCGCCCTCCAGG	-	4680
4681 -	TTCGAGGGATTCTCATGAGGCTGTTTTTTAATGAGACAGGGTCTGCTCTGTC	-	4740
4741 -	ACCCAAGCTGGAGTGCAGTGGGAGTCAAGCTACTGCACCCCTCGAACTCTGGTCT	-	4800
4801 -	CAAGCAATCTCCACCTCCCTGGTAACCTGGACTACAGGTGCCACCATGCCAGC	-	4860
4861 -	TAATTATTTGTGAGAGATGGGTTCTGCTATGTTGCCTAGGCTGTCTGAAACTCCT	-	4920
4921 -	GGCCTCAAGCAATCCTCCAGCCTCAGCCTCCAAAACTCTAGGATTGAGGCTGAGCCA	-	4980
4981 -	CTGTGCCAGACCCCTGCAGGAAGCTCTGGGTCTTAAGTGTGACACTCAGGTGTCAGC	-	5040
5041 -	ACTTAAACAAGTGTCCAAATGGGTTGATGCAGGTAAACCAAGAAAGATGTTGAGAAAG	-	5100
5101 -	ACCTGAAACTGGGGCTTCTAATGGGTCAAAGCCAGGGATACAGGTTGGATTGAGTA	-	5160
5161 -	GAATGGGAAAACCTGCGGGTGGGGAGGGGTTGTGAGGGATTCCAGGCAAAGGCCCCCTT	-	5220
5221 -	CTTCTTCAGCAGAGACCAAGTACAGAAGGAGCAGCTGCCAAGGCCATGCCACCTTCT	-	5280
5281 -	TACAGATGTGAGCCCTACTCCTGTACCTGGAGGCAGCCCGAGAACGATACCCCCCA	-	5340
5341 -	TCTATGGACCCCTGCAGGAGCTGGTCCGAAAGGGGGTGTGAGGTTCTAGACCCCCA	-	5400
5401 -	CGCCCCTTCTCTCGCAGCTCTGAGCTGTGGGATGGTGGAGGGGAGGCCACTCCT	-	5460
5461 -	CGCAGGCCAGCTGATCTACTGTACCCCCCTCTGTATGCAGCTGTAGAGATCTCCAA	-	5520
5521 -	CAGCTGACCCCTGCCTGGAACAGCTGGTCTCATGTACGCTTGGGTTCTGGAC	-	5580
5581 -	CTGGAGGAGATGAACCCCTTAGTAAAATGGTAGGAGACTCAGATGGGGATGAAGGA	-	5640
5641 -	GTCCAAGGCCAGCCTCACCCCTCCATTCTCATGTCTGCCAGCATCTCTGTTCT	-	5700
5701 -	TTGCCGGAGGTCTCCATCAGCCTGCCCCATGAGGTCTCCATCTCAGATACTGTGCC	-	5760
5761 -	AACCGCCTACACTGCCAGCCGCTCCCCCGTACCTCTATAAGAAGATGCGTGGCACCT	-	5820
5821 -	GGAAGCCACCCAGAGGCCCTGGTCGGGACAAGATTCCCTGTGGATTAGTAAGTCT	-	5880
5881 -	CTTACCCAAATCAAAGTCTCCCCCTTCTATGATGAATGCCAATATGACCCTCAAACCG	-	5940
5941 -	TCACCAGCAAAGTGAAGTGAAGCCAGGGCCAGGCAGTGGCTACGCCCTGAAATCCCA	-	6000
6001 -	ACACTTGGGAGGCCAGGCAGGAGTCACTTGAGCTCAAGAGTTGAGATCAGCCTGG	-	6060
6061 -	GCAAGATGGCAAGACCCCTGTCTACAACAACAAAGAAATTGCCAGGCGTATGGCTGGC	-	6120
6121 -	CTGTAGTCCCAGCTACTGGGAGGCTAGGCAGGAGGACTTGAGGCCAGGAATCAAG	-	6180
6181 -	GCTACGGTGAAGTGTGATTGTGCCACTGCACTCCACCTGAGTGGAAAGCAATAATCTGTC	-	6240
6241 -	TCTTAAAAAAAGTGAACCCAGGAAACTAAAGGCTTGTGAAAGGCTACCTCTATT	-	6300
6301 -	TTCTTAAACCCACCTCCACCAAAATAAAAGTCTCATCTTAAAGTAGGCTGGCAGG	-	6360
6361 -	GAGAAAAGGCCCTGGAGTCACATTCTACCTGAGAACTTCAGGGCAACTCTGATGAGTT	-	6420
6421 -	CCCACCTCAACTCCAAAATTAAAGCCCTCAACAGAAGTAGCTAGGAAGCTGATCACTTCT	-	6480
6481 -	AATTACAGCTCCCTCCCCCTAGCTACTTTCTGTCTATCGAGATACTGGGAAGACAC	-	6540
6541 -	AGGCCAGAGTCCAGCCAATTGTCGCCCCAGATCCAGAAGCTGTGGCCATGCCGATG	-	6600
6601 -	GGTCCCCCTAGGACCAGCCGAGGATGACCTTATTCTATGGTAGGAGCTAGGGCAATAGCA	-	6660
6661 -	ACGTGGGCCTGGGAGCTGGAGGGGAGGCAGAACCCACCAAGACAATCCACCTCCCA	-	6720
6721 -	AACACTTTGCTTCCCTTAGTAGTGTGATAGCATTATTGTGCCCTGAAAGCAGTCATGC	-	6780
6781 -	AGACCCCAGTAACAACCCATGGAGATCTATGCTATTGGCCCCATTAAACAAGAAAACAG	-	6840
6841 -	GGTGTCAAGAGAAGTGTACCTGCCAAGGACACACAGCTAGCAGAGCGAATGGACAGG	-	6900
6901 -	TCAGGACCAGTTATTGAGCCATTACTAAGTCTGATCAACAAGGAAACA	-	6960
6961 -	AGTTCCCCGGGGTTTCCCACCCGAGCTGAAACAAAGCCTTTCACCTGAGCCT	-	7020

Fig. 23 (continued; 6/6)

7021 - CTCACTCAAAGGGAGGGACTCCCGAGGGGCAGGGGCACTCAAGTCCAGGCCTGTCTATC - 7080
7081 - CCTGGCCCCCCCACCCCAAGGATTGTGCCCGACCGCTTGGGACTACCAGCAGCTGCT - 7140
7141 - GACCATCGGCTTCGAGGAGCCCACGCCACGCTGGCCACCGACCTGCTGGTGCAGATCCT - 7200
7201 - CACGGGCCAGGCAGGCCAGGCCGGCCTCCGAGCGCAGCCGGCCTGCCGGGTGGCAGC - 7260
7261 - GCAGGGGTCTTGAACCTGGGAAGAGGGTAGGAGCTGGAACTTGACACTTCAAACCTCCA - 7320
7321 - GAATAGGGGGCAGGGGAGGGCTACTCGTCTCGCAGTGCAGCCGGCCTCGCCTTCCA - 7380
7381 - AAGGGCCAGGCCGAGCTGACCTGTCTGCACCGAGTCCGGCTGGCGTGGGCCCTGAAT - 7440
7441 - GCGGACACGTCAAGTTGTGTTAAATAAAAGAAAGAAAGAGGTACAGGCTCAGCGTCCG - 7500
7501 - CTGCGAATGCCCGCCCCCTCCCCGGGGATTGCCCAACCGACTCGCTGGCCTCTGGG - 7560
7561 - AAATGTAGTCTTGAAAGAAGCCTGAAATTGCCAATAGGCGGACGAGAGTTGGCGCA - 7620
7621 - TGCATAGGCCACATGAAGCAAAAGGGAAAGTGGTCCCCGTCAACACCGGAACCCAGA - 7680
7681 - AAACTGCAAGTTAGGGTACCGGGAAATTCAACGTCACGGAGGAAGAGACTTAAGGC - 7740
7741 - TACGCCACTCCATATTGACCCGAAGTTATTAGCGTAGAAGACTACTTTT - 7800
7801 - CCCGACGCCAGGAAAGTGCCCTCGATCAGTTCTAAGGGCCCGAGTTAGACTTTT - 7860
7861 - TTTTCTTCCAGTTGGGACTGGGGCCGGACAGGTCTGCTTTCTGGGTA - 7920
7921 - TCCGGGGTGCAGACAAGGTGGGAGAGCCCTACGGTATCCAAGCTT - 7965

Fig. 24 (1'9)

1 - CAACATGCTGGGACCAGAAGTGTTCAAATTGGATTTCTCAAATTTACCGGTGA - 60
 61 - GCTTCCCCAATCTGAAAATCTGAAATCCAACATGCACGGCTCTGAAGTCTTCAGCAGC - 120
 121 - CTTGGGGAAATATTAACATCCTAACAGCCCTAACCAACGCTCAATTAGCACAAACAG - 180
 181 - TTTACAATCTCTACCCACAGCCTGATGGAGGCTCTGGGACTAGACTATTTAGCCAA - 240
 241 - CAGTTCTGCAAAATTAACACTGACTTATAAGTAAATAGTAATTCAACACCTCACTGCTAA - 300
 301 - TGCTGTAACAACCTCTGCAGACCTAGGGAGCAAGTAGCGTTGCAGAGCAGTGGAAGGCT - 360
 361 - CTGAAGTGAACCTTGAACGGCCTCAAAAAATTGGGTTGGCAAAAGTCAAATCTCT - 420
 421 - TAGGCTTCAAATTCCAGGCACAAGGATTGGGTTGATTTCAATTATCCAGAAGCAATG - 480
 481 - GGGATAACAGAATTGTGATCTCATGTGAGGGAACTGTGGGGTTTTCTACTTTAACCC - 540
 541 - CAGTGAGACTTTGAGGTGAGGGTAGAGAAAAGGCTCATGAATATGCCGAAGCCTAA - 600
 601 - CTCAGCACCTTCTGAGGAACGTGACTGCCAAAATGTTAATGGAGAGGGAAAATATGACC - 660
 661 - TACTTCAAACTGACTGCCTCAGGGAAACCTGCTGTGGTAGTGTCTCTGG - 720
 721 - GTGAAAGACCAAGGTAATTACCTGGGTGCTGGTCTCAGACTTACCAAGTTGAATCCCTGT - 780
 781 - TTTAACCACTCACTATCGATATGACCTGGATAAGTACCTAACCTTCTTACTGTCC - 840
 841 - TTTTCCGTAAAATGGGATAACAGATAGTAGTTATTCTATGAGTGGTTATGAGAACCAA - 900
 901 - GCTATTAGATAGCGGGAAAGCACACAGTAAGCGTTCAAGGAACGTCTATTGTTATTAAA - 960
 961 - GCCTCCTTGGAAAGAAGGACATTGAGGCCAGAGAGAGAACAGAACGTCCAGCCACACAG - 1020
 1021 - CAAATCCGTGATGAAGTTGGACTGGAGTATGGGTCTCAGTCTCAGGCCAGGACTCT - 1080
 1081 - ATCCCTCTCCGAGTCCTCGGAGTTCCCGATGGAGTCACATTGTCACGGCCAGGGA - 1140
 1141 - GGAAGGTTGATGGAGGCCTGAGGAAACACAGCCAGGCGCAAGGTTGGAGTTGAA - 1200
 1201 - GCATAGCTTCTGCGAGATAGAAACAAGGTGACATGGCACTCGTGCAGAATGACGGCT - 1260
 1261 - CCTTTGGACTCCCAGGACTACAGTCCCTATGCACCTGGATCTGCCAGCTAGCCCTG - 1320
 1321 - CGTAAAGAGGGACCGTAGTCTTCCCTGCCCGCCCTGCCGGGCGCCCGCTCCGAG - 1380
 1381 - GCGCCCTCGCTTCGCTCCAGCAAGCTCCGCGCCGGCGCTATTGATTGGCTG - 1440
 1441 - AGGCAGGGAGCAGGCCGCTGGCCGGCAGCAGTTACTCGGGTTTCCGGTGCAGGCCAGAG - 1500
 1501 - GTGGGGAAAGCCATCGGACGTGGCGGTGAGGTACGTGCAGCGGGCCGGTGGCGAGAC - 1560
 1561 - TATTGAGAGTGTGCGGGCCGGGATGTTCTGGCCTGTGGGGAAATCACGCCAACTCCCC - 1620
 1621 - GCGTGGGCCGGGGCTGTCTGGGATATGCGCATGCGCGGGCGTGCCTCGGGCTTGAGG - 1680
 1681 - GCGCGCGGGCGTGGTGGCTGCGCGCGGGGGCGCACGTGGGCCTGAGGGCGGG - 1740
 1741 - GCGGTGCCGGAGTCCGCCACGTCACTCTGGCCCTGAGCCAATCCCCGCCGGCCT - 1800
 1801 - GCGCGAGGGGGCCGGTTGTGCCGGAAAGTGGCTCCAGGGAGAACGGCTTCCCTCA - 1860
 1861 - CCCGCTGTGGGAGCTGCGCCCCGAAAGCTGCCCGCACGTGGCTCTCTGACCCGC - 1920
 1921 - CAAGACCAGAGAGCCGTTGGGCCCTCCGCCGGCCTGCCGGTCCGTTATTTAAGAA - 1980
 1981 - GCTTGTCGCCTGCTGTGGGATTCTGATCCAGGCTGCGAAGAATTGAGTCTGGA - 2040

 2041 - AAATAGCAACTGTGTTGTTCTAAAGGATCTCTCCTGACCCAGCATCGCTCATCACAA - 2100
 - M

 2101 - TGAAGAACCAAGACAAAAGAACGGGCTGCCAACAAATCCAATCCAAAAGCAGCCAG - 2160
 - K N Q D K K N G A A K Q S N P K S S P G

 2161 - GACAACCGGAAGCAGGCCGAGGGAGGCCAGGAGCAGGCCAGGCCAGGCGGCTCTGCAG - 2220
 - Q P E A G P E G A Q E R P S Q A A P A V

 2221 - TAGAAGCAGAAGGTCCCGCAGCAGCCAGGCTCTCGGAAGCCGGAGGGTGTGCCAGC - 2280
 - E A E G P G S S Q A P R K P E G

 2281 - TCTGCGTTGCCAGCGGGCAGGGGAGGAGCTGTGGGTCGGCTCGCTTGACTTACA - 2340
 2341 - GGCGAGGCCAGGTGTCGGAGGAGGAGATGAGAATGAGAGGACAGTGTGGGGCC - 2400
 2401 - GCGGTCCCCCTCGCCTCTGGCGAGTTGGCGAGCTGCCCTCTAAGCACAGGAACAGA - 2460
 2461 - GTTCTGGAGAGAAGCTCCGACGGGATTAAGTCAGGTGGCAGCCAAACGAGGCACCCAGTC - 2520

Fig. 24 (continued; 2/9)

2521 - AGGAAATCCAGGTCCCCTAGAAAACACCTCAGCCACCAGCAGCTA	ACTGCCCTTCCTGTT	- 2580
2581 - TGAGGCATTCTAGAATGATCTGAATGGCAAGAAATGGTTTGTGGGGGGAAAGGAGAT	- 2640	
2641 - GGACTAGAAGTTGCTCCGTGCCATCCCTGTGTGCTGATGCTTACATACTTTATGATCT	- 2700	
2701 - AACAAATATGTCGGGTGGTAGTGAGAAATAGTTGTGTCATTACAGTAAACAGACTT	- 2760	
2761 - AAAGAACGTTAGGCAACGATTACTATAATTCTGATTTAAAGATGTTCAATCTAAAT	- 2820	
2821 - TCTGACAGGAACTAGATTGCTGAATGATACTCCATCTTGCTCTCAGTTCCATAAAA	- 2880	
2881 - AAAAAAGTTAGGCAACATTAACTCAAACGATGAGTTGGCTGGCCTGAAAATCCCA	- 2940	
2941 - ACCAGTGGTATAATCGTCTTCTTCTACTCTACCCCTCATCCTCTCCTGCTGTAGGGC	- 3000	
3001 - TCAAGCCAGAACGGCTCAGTCTGGGGCCCTCGTGTGCTCTGAGGAGCTGAGCCGCCA	- 3060	
3061 - Q A R T A Q S G A L R D V S E E L S R Q		
3121 - ACTGGAAGACATACTGAGCACATACTGTGTGGACAATAACCAGGGGGCCCCGGCGAGGA	- 3120	
3181 - L E D I L S T Y C V D N N Q G G P G E D		
3241 - TGGGGCACAGGGTGAGCCGGCTGAACCCGAAGATGCAGAGAAGTCCCACCTATGTGGC	- 3180	
3301 - G A Q G E P A E P E D A E K S R T Y V A		
3361 - AAGGAATGGGGAGCCTGAACCAACTCCAGTAGTCATGGAGAGAAGGAACCCCTCCAAGGG	- 3240	
3421 - R N G E P E P T P V V N G E K E P S K G		
3481 - GGATCCAAACACAGAAGAGATCCGGCAGAGTGACGAGGTGGAGACCGAGACCATCGAAG	- 3300	
3541 - D P N T E E I R Q S D E V G D R D H R R		
3601 - TGGTAGGCTCCTGTGCCAGCCAGTACTACCTGCTGTGACCTGGGTGTGCCCTCTCC	- 3660	
3661 - TCTCTGGGTCTAGTTATTTCTCTTACAGTAAGAAAATTAGACTAGGCCAGAGTTG	- 3720	
3721 - AAAACCCAAATATCTGCATAAGCTGGCTGGCATGGGCCACCTGAAGATGGAGGCTT	- 3780	
3781 - TACTGCTCCCTGATTAGTTGCTCTCACTAGCCAAGTGAGAGCAGGCAAAACTACAGGCT	- 3840	
3841 - GGGTGCAGTCAGGCTTTTTTTTTTTTTAAATAAAGAAAAGCCAGAAATCT	- 3900	
3901 - AGAGTTATGTGAGAACTCTAGATTTTCATAGTTAGCAGCTAAAATGGTAAGAGCCAAA	- 3960	
3961 - CAAAACCCATCCGTGGTTGGATTGGCACACATGCTGCAATTGCAAGTCATGCCATGCTG	- 4020	
4021 - ATCTCTGGGCCCTCTGGGGAGGCAGAGGAAGGCTCCCTGACTCAGTCACAGGAATG	- 4080	
4081 - GGGAAATAGGCAGTCAGTCATTTACAGCAGGGTATGTATTTAAGAGTCTAGGCCGG	- 4140	
4141 - GGTGTGGCTCACGCCTGTAATTGCAAGCAGTCTGGGAGGCCAGGGGGATCAC	- 4200	
4201 - TGAGGGTCAGGAGTTGAGAACAGCCTGGCAACATGATGAAATCCGTCTACTAAA	- 4260	
4261 - ATACAAAAATTAGCTGGACATGCTGGCACAGCCTGTAATCCAGCTACTGGGAGGCTG	- 4320	
4321 - AGGCAGGAGAACGGCTGAACCCGGAGGGCAGAGGTGCACTGAACTGAGATTGTGCCAC	- 4380	
4381 - TACATCCAGCCTGGGTGACAAGAGTGAAACTCTGTCTCAAAAAAAAAAAAAGAATCTA	- 4440	
4441 - GAATCTAAGTCGAGTGTCAATTATCCATGTTTATTCCTATCCCTTTCCCTTATGT	- 4500	
4501 - ATCCTCTTACTTTAAAGAGGAACCTTAAAAATCTTAGGGACGACTAGGCAGAGTGGCTC	- 4560	
4561 - ACACCTGTAACTCCAGCACTTGGGAGGCCAGGCAGGAGATTGAGGTCAAGGAGTTC	- 4620	
4621 - GAGACCAGCCTGGCAACATGGTGAACCCAGTTCTACTAAAGATACAAAAATCAGCC	- 4680	
4681 - GGGCGTGGTGGCACGTGCCTATAATCCAGATACTCGGGAGGCTGAGGCAGGAGAACATCAC	- 4740	
4741 - TTGAACCCGTGAGGCAAAGTTTCAGTGAGCTGAGATCATGCCATTGCACTCCACCTGGG	- 4800	

Fig. 24 (continued; 3/9)

4801 - TGACAGGGT GAGACTCCATCTAAAAAAAGAAAAAGGAAAAAATCTTAACGT CACATACA	- 4860
4861 - TGGAAAGATCATCTTTCACCCCCCACCCCAACTGAGATGGAGTTTGCCTTGTCAC	- 4920
4921 - CCAAGCTGGAGTGC ACTGGCGGATCTAGCTCCCTGCAAGCTCCGCCCTCCGGGTT CACA	- 4980
4981 - CCATTCTCCCTGCCCTCAGCCTCCCGAGTAGCTGGACTACAGGCTCCTGC TACCATGCC	- 5040
5041 - GGCTAATT TTTGTATTTTTAGTAGAGACGGGTTCATCTGTGTTAGCCAGGATG	- 5100
5101 - GTTTGATCTCCTGACCTCGT GATCCGCCGCTCAGCCTCCCAAAGTGCTGGATTACA	- 5160
5161 - GGC G T A A G C C A C T G C A C C C C G C T T T T T T A A T T A A T T T T T A G A C A G A G T C	- 5220
5221 - TCGCTCTGCCCAGCTGGAGTGCAGTGGCGCAGTGGGCTCACTGCAACCTCCGCTC	- 5280
5281 - CTGGGTTACGGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGACTACAGGCTCCTG	- 5340
5341 - CTACCATGCCCGCTAATT TTTGTATTTTTAGTAGAGACGGGTTCACTGTGTT	- 5400
5401 - AGCCAGGATGGTTTGATCTCCTGACCTCGT GATCCGCCGCTCAGCCTCCCAAAGTCC	- 5460
5461 - GCCTCAGCCTCCCAAAGT GCTGGGATTACAGGCGTAAGCCACTGTACCTGCCTTTTT	- 5520
5521 - TTTAATTAATTAATT TTTAGACAGAGTCTCGCTCTGTCAACCAGCTGGAGTGCAGTGG	- 5580
5581 - CGCGATTGGGCTCACTGCAACCTCCGCTTCTGGGTTCAAGCGATTCTACCTCAGC	- 5640
5641 - CTCCGGAGTA ACTGGACTACAGGCCGTGCCACCAACACCAAGCTAATT TTTGTG TAT	- 5700
5701 - GTCTT TAGTAGAGATGGGTT CACCATGTTAGGATGGTCTCGATCTCTTGACCTCGTGA	- 5760
5761 - TCCGCCTGCCTCGGCTCCCAAAGTGCTGGATTACAGGCATGAGCCACCTTGCC	- 5820
5821 - GAAAGTATCTTCA TTTAAAGTCACTGTTGGCTACTCTGTTGACAAGAGTTAGTATT	- 5880
5881 - TCTCAAGGAGGCTAAGATA CCTATT CTTGGATCCTACCTCTATCAGGAGGGTGGC	- 5940
5941 - CTTCCTTG CATTGAAACAGTATGAAAACAGTAGCCCTGAATT CATAAGTGGACACCTT	- 6000
6001 - CTTCTATTGGTAGAGCAGGCAGTTTTCTCCTGCCAATGGTGCCTACTAAGGAGATT	- 6060
6061 - CACTAGGGTACAGTCGTTCA TTGATAAGCATTGTTGAGCATACTCTGTGATGGTAC	- 6120
6121 - TATGGACAGTACTGGGCTATAGTGAGGGCAGGATTGAGTTGGCCTTATGGCAAGGAAG	- 6180
6181 - GCAGCTAATCAACAAGCAAATATAAAGTATGATGGGAGGGCTGCTTCAGCACTCATG	- 6240
6241 - AGTGTGAGCCCAGGCCTGGAGGGACACCTGGAGAAGAGGGTGCATGTCTTGCTCCTGT	- 6300
 6301 - GCTTT CAGGGAAAGGAGATCACGTTGCTGATGCAGACATTGAATACTCTGAGTACCCAG	- 6360
- K E I T L L M Q T L N T L S T P E	
6361 - AGGAGAAAGCTGGCTGCTCTGTGCAAGAAGTATGCTGA ACTGGTCAGTTCCCCCTCCGCG	- 6420
- E K L A A L C K K Y A E L	
 6421 - GGCACCTCCCTGCCGTGGAAAATCAGCATGCCACCTGGTGTAGGTTGGGGTGCAGA	- 6480
6481 - GTCAAGTAGGTGGCTTAATTCTGTTAGCTTTCTCTGAACATATCTGTTAAATGGGAA	- 6540
6541 - TCACTCCAGCCAGCCTCTCAGGCTGTGCAGCAAGAGGAGAAACTGCATATTCTGTG	- 6600
6601 - AAGAAATTCTCAAAGAATGATTCCAAGGTGGTAGAGGCCCTGTTCCCTGGCTGAGTCCA	- 6660
6661 - AGACACCTTGTGATCTGATGCTCTTCCCTCAAATACAGATGCATAGAGCCATTATCACA	- 6720
6721 - GTTAATAAAACTAACACTAGTCACTTGATACTTTCTTTACTCCAGAGCAGTCTCT	- 6780
6781 - TGTCACTGCCCTCTCATATTCCCATGACATTGACTTTAACAGAAACTAGACTAGCTGT	- 6840
6841 - CTTGTAGGATGCCCTCTAGCTTGTCATCTCTGTTATCATTTACTCTTACCT	- 6900
6901 - CCTGGTACATGTAAGTGAAGTAGAAGTTAGCTCAAAGCTTGCATCCAATTCTGTTAAC	- 6960
6961 - TTTTGACAAGAATTCTCATAAGTACTTCATGTTCCATCACAATAATGCAAAGCATGC	- 7020
7021 - TCTTCCCACTTGTGTAACATTGTCAGTGGGTTGGGGTGGGCAGCCAGATTCTTCC	- 7080
7081 - ATCATCAGGTCCCTGTGTCAGAATTGAAACTAACAGATTATCCATTGATGGTCACAGCCT	- 7140
7141 - GTGTATGTATGTATGTATGTATGTATGTATTTATTTATTTATTTGAGAC	- 7200
7201 - GGGGTCTGCTCTGCCCCAGGCTGGGTGCAGTGGCACGATCTGGCTCGCTGCAAGC	- 7260
7261 - TCCGCCTCTGGGT CATGCCATTCTCCTGCCCTAGCCTCCCGAGTAGCTGGGTCTACAG	- 7320
7321 - GCGCCCGCCACCATGCTAGGCTATT TTTTTTTTTAGTAGAGACGGG	- 7380
7381 - TTCACCGTGTAGCCAGGATGGTCTCGATCTTGACCTCGT GATCCGCCGCTCGGCC	- 7440
7441 - TCCCAAAGTGC TGGGATTACAGGCTTGAGGCCACGCCCTGGCTATT TATTATT	- 7500
7501 - CAGAGTCAGAGTCTCGCTCTGTCACCAGGCTGGAGTGCAGTGGCGCAGTCGGCTCATT	- 7560
7561 - GCAACCTCCACCTCCCAGGTTCAAGCGAGTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGA	- 7620
7621 - TTACAGGTGCATGTCACCATGCCCTGGCTAAATTGTATGTTAGTAGAGACAGAGTT	- 7680

Fig. 24 (continued; 4/9)

7681 - CAGTATGTTGCCAGGATGGTCTTGATCTTGGCCTCGTATCCGCCGTCTCAGCCTC - 7740
 7741 - CCAAAGTGTGGATTACAGGTGTGAGCCACTGTGCCTGGCTCTAAGTATTATTTAA - 7800
 7801 - AATTAATTCACTCACACATTTATTAAATATTTCTGTAAAGGAACCTTACTCATCTT - 7860
 7861 - AAAATGGGAATGTCTACCTGCCAATGACATTCTGTAAAGGATAAATAAAAGGTATA - 7920
 7921 - AGGAAGATAAAGCACCCCTTGGAGTGATCCAGCCAGGGAAAATTGCTGATGCAAGAGAG - 7980
 7981 - GAAATGAGTTGCTAGAGTGGTGTGAGTAGAGGAGGGAGCTGAGGCCGTGCCAAGAA - 8040
 8041 - GGGGGCTTGGCTGTGTAACCACATGGCTAGGTCTGTGACTGGAGGAGAGGACGGGC - 8100
 8101 - AGGTGGACTGGTAGATGTGCAGCTGTGCCCTGATTCTCTAGTTCTGTGTTTGA - 8160
 8161 - GATTTGATGAGAACGATGAAATAGTTGTCGAAAGGAGAGGTGTGAATAGCATATGCA - 8220
 8221 - TTGTATTGGGATTGCTGGCTTCCGTGAAATTGGTGGCCATGAATTAAAGTGAGACTCTT - 8280
 8281 - CAAGTAGGGTTGTATAGTACTGGTGTAAAGCAGGAAGGTGCTTACTAGGGTTGCAGTA - 8340
 8341 - CTACTGGGAAAGGCCAAGAGAGTTGAGGGTGTAAAGAAATCCAAGCCAGGTATGTAGTT - 8400
 8401 - ATTTAAAGGAGAGTGGAGGATGGTCAATGGATTGGAGGTCTATAGGGTAAGA - 8460
 8461 - GACTTCTGAGGATCACAGATACTGATTGAAATGAGCTAAAAGATAGGTGATGGTAGTC - 8520
 8521 - CTGGACTGGGATGCTGGAAATTGAGATAGTGGGTGTGCTCTGGTAGTGTACAATCTAG - 8580
 8581 - ATCTCGCTGTCCAAGATAAATTGCTCTAGCTAATTGACATGTGCCAGTTGAATT - 8640
 8641 - GAACATGCTATAAATGTAAGATACACATCAGCTTGAAGACTTAAGCAAAACAAAGAA - 8700
 8701 - TATAAAACATCTTTGTGAGAGAGTGTCTCAGTCACCCAGGCTGGAGTGCAGTGGCGTG - 8760
 8761 - ATGTCCTGTTCCAGGTTCAAACGATTCTCCTGCCACAGCCTCTGGAGTAAGTGTGAGA - 8820
 8821 - TTACAGGCGCATGCCACCAACTGGCTACTTTTGATTTTTAGTAGAAACAGGT - 8880
 8881 - TTCACCATGTTGCCAGGCTGGTCTTGAACCTCTGACCTCAAGTGTATGCCGTGCTCAG - 8940
 8941 - CCTCCCAAAGTGTGGATTACAGGATGAGCCACCACTCCGGCCTACTTTTACAT - 9000
 9001 - TGATTCCGTGTTGAAATTGTAATGTTGATATTAGGTTAAATACATATATTACTAAA - 9060
 9061 - TTAATTTCACCTGTTTTACTTTTGTGAGGAGCTGGCTCATGGGAGGGAACTGAG - 9120
 9121 - GTGGTTGCATTATATTCTGTGTACAGGCTGGATAGGGTCATGGGAGGGAACTGAG - 9180
 9181 - CTGGGAAAGGAGTGGGTTGTGGAAGAGGGTGTGGACTGTGAGGCCAGGGAGTTAGAAG - 9240
 9241 - GATTATCTGTTGATACTGAAGTGGCCACAAATGAGAAAAGTAATTGTTGGAGAGCG - 9300
 9301 - CTGATGAACGCAGCGCTAACGTTTGAGGAATGCGAGGGAGCGATGGGGCTGTCTGT - 9360
 9361 - TAATAGGCACAAGGTACGGTAGGTGGCTCATCTGGGAGTGTCCAGCAAGT - 9420
 9421 - TGGGAAATGCAACAGCTTGAAGTGGCTTAGTGGCCCAGAGTCAGAGCTGAAATAGGAA - 9480
 9481 - TTGGCATCTGCTGGCTGTGTCGGCCCTGCTTGCCCTAGTGAGTTACCATTTCTGTCCC - 9540
 9541 - TACGGTGGAGCCTTGGGTTATTGTGAGTTCATGGGAGGAGCGTGTAAAGCACCGGCACA - 9600
 9601 - GCATCAGCCATGAGAGTGCTCTGGCTGAGAGGGTAAGGGTCAGGGCAGCTCAGGAGA - 9660
 9661 - CCCTAGACCTGCATAGTGTACCCCCCACCAGGAAGGCCACAGATGCTCACCTGCCCT - 9720

9721 - CCCTATCCCTGTCCCCAGCTGGAGGAGCACCGAATTACAGAACGAGATGAAGCTCCTA - 9780
 - L E E H R N S Q K Q M K L L

9781 - CAGAAAAAGCAGAGCCAGCTGGTCAAGAGAAGGACACCTGCCGTGAGCACAGCAAG - 9840
 - Q K K Q S Q L V Q E K D H L R G E H S K

9841 - GCCGTCCCTGGCCCGCAGCAAGCTTGAGAGGCTATGCCGTGAGCTGCAGCGGCACAACCGC - 9900
 - A V L A R S K L E S L C R E L Q R H N R

9901 - TCCCTCAAGGTAGGCCTGGCCCCCTGGAACAGGTGACTCTGGTTCTTGACTTCCACT - 9960
 - S L K

9961 - TAATGTTCTTCATGGCTTCCCTTTAAAGTAGTGCAGGCTAGGGCCAGGCGCAGT - 10020
 10021 - GGCACACATAAGTGATTAAGGAACTTCTGCCACTAAAAACAGAAATTAAATTTAGTAA - 10080
 10081 - TATACTTAACCCAATATCCAAACATTACAATTCACATGAAATCAGTGTAAAAAGCA - 10140
 10141 - AGGCTGGGTGTGGCTCACACCTGTAATCCAAACACTTGGGAGGCTGAGGTGGATGG - 10200
 10201 - ATCACTGAGGCCAGGAGTTGAGACCAACCTGGTCAACGCAGTGAAACCCATTCTACT - 10260
 10261 - AAAAATACAAAAATTAGCCGAGTGTGCTGCCAATGCCTATAATCCCAGCTACTCAGGTG - 10320

Fig. 24 (continued; 5/9)

10321 - GCTCAGGCATGAGAATTGCTTCACCTGGGAGGCTGAGGTTGCAGTGAGCCGAGATTGCA - 10380
 10381 - TCACTGCATTACAGCCTGGCAACAGAGTGAAGACTCAGTGTCCAAAAAAAAAAAGTA - 10440
 10441 - GTGCAGGCTTGTGGCATAGAAATACACTTCTCAATAATGCCTTACGTTAAGAGAGTACT - 10500
 10501 - GCTTGTAAATCATTGACATGTATTAGATAAGGTGAAGGATAAAAGTACTAAGAGAATCCAT - 10560
 10561 - AATGCACTGGCGTTAGTATTCTCAATGAAATGACAGTCCCCTGGTAAGCGGAGGCCTGG - 10620
 10621 - CTCTGACAAGCAGCTTGTGCCAGACGTGGTCAGTCAGGAACCTGGGTCTTCCCATG - 10680
 10681 - TTCTGCTGCTTCTATGGTGAGGTCACTGTGGTACACCAAGTTAAATACAGCCTTT - 10740
 10741 - AACTTTCTTTTATGTAAAATCTTACATGTAGTTAGAATGAAATTATTATACAT - 10800
 10801 - GTACCATTTCATATCCTGTGCCCTTTTCACTTACATAACATTTCCTACAGTAT - 10860
 10861 - GTGTAGGGCTATCTTCTCATTATATGGATATATTATCAGTGCCTAGTTAAAGCATT - 10920
 10921 - TGGGGGTTGTTACAAATTTCATTACATATAGAACTATAGTGAAAATTCTTGTAT - 10980
 10981 - ATTTATCAGGGTCAGTTATAGAACTTATCTGAGGATAAGTCATGAAATTGAAATGG - 11040
 11041 - CTAGGTACAGTATATGCAGATTTCATTTAATAGATTTGCTGGATTGCCCTCCAGT - 11100
 11101 - GAGGGGGCAGTGTGCCCTCCCCATCAAAGTGTGAGTGCCTAATTCTGCACAACTTGC - 11160
 11161 - AAACCCCTGGGTGTTACTAAATTAAACAGCTGGTCTCTGGGGTACAGAGGGGACAAT - 11220
 11221 - GCACATTAAATCTGAAATCTGGAAGAATAGGCCTTAGGAGATCCGACTTGCTCAGAATGG - 11280
 11281 - CACTTAGCACTTACATGTGTGCATGTGCCTGCATTTCCTTCTTCTTCTTCTTGT - 11340
 11341 - GGGACGGAGTCTTGCTCTGTGCCCATGCCAGGCTGGAGTGCAGTGGCGCATAG - 11400
 11401 - CTCACCACAAACCTCCGCCTCCAGGTCAAATGACTCCTCTGCCCTCACCCAAAGCAG - 11460
 11461 - CTGGGACCAACAGGTGCACACCACGCCGCTAAATTGTATTTAGTAGAAACGGGG - 11520
 11521 - TTTCACCATATTGGCAGGCTGGCTCAAACCTCCTGACCTCGTGCATCCGCCACCTCAGC - 11580
 11581 - CTCCCAAAGTGTGGATTACAGGCGTGAGCCACCGCGCCTGCCATGTGCCTGCATT - 11640
 11641 - CTAGGGGAGAATCTCACTGATGTCACCTGATATAACAGAGGGGCCATTGAAACCGCA - 11700
 11701 - TTGCACAAACATCCTGGAGTCTGGCTACTCCACGCTTGGAGCAGGGAGGGCTGTTGGCA - 11760
 11761 - GAGACCATCTGTGGACTAGCTGGGACCCCTGTGAGGTAGCAGTGGATGATGGCTCTCG - 11820

11821 - GGCTGACTTCTTGCCAGGAAGAAGGTGTGCAGCGGGCCCGGGAGGAGGAGGAGAAGCG - 11880
 - E E G V Q R A R E E E E K R

11881 - CAAGGAGGTGACCTCGCACTTCAGGTGACACTGAATGACATTAGCTGCAGATGAAACA - 11940
 - K E V T S H F Q V T L N D I Q L Q M E Q

11941 - GCACAATGAGCGCAACTCCAAGCTGCCAACAGAGAACATGGAGCTGGCTGAGAGGCTCAA - 12000
 - H N E R N S K L R Q E N M E L A E R L K

12001 - GAAGCTGATTGAGCAGTATGAGCTGCGCGAGGAGGTAAAGGTATCACGGACAGCAGTCAT - 12060
 - K L I E Q Y E L R E E

12061 - GGCCCAGAAATTGTGAGGTTTGAGTGTGTCTAGGCAGTGGACAGTACCTTTCAGGC - 12120
 12121 - TTCATCCCATTCTCCCTTCTTCTCCTCCTCCTGGAGGAGAGTAATGTTATTCC - 12180
 12181 - TCATAGATAAAAAACAGGTGTGGAGAAGAGAGACTCAGTACAGCCACACAGCCCCAGGTCC - 12240
 12241 - ACAGTGCCTTGTCCCAAATGACTGGGCCAGGCATCTTGGAAATTAGAACTATCCACATT - 12300
 12301 - TTAGAATGGAGGTACATGTATGGACTGTGTATATAGCACCCCTAGCAGGGCCTGG - 12360
 12361 - GAAGCCAGACACATTAATGTATTAGCAGTAACTCCAATACTCACCTACATTATG - 12420
 12421 - GGCTTACAATGATGCAGGTCAAGTCTGGCTGCCAGCTTATGACAATTCCATTTCAGAA - 12480
 12481 - CTTTGTAGAATTGGAATTGCAAGGGGAGGGGTGTACCTGTGATCAGTGGACTCCAGA - 12540
 12541 - GACTGTGTCACACTGATTCTGCTCTGCCACTAAAAGGCAGAATTATCAGGCTG - 12600
 12601 - GGCCTGGTGGCTCATGCCTGTAATCCCAACTTGGGAGGCCAAAGCGGGCGGATCACC - 12660
 12661 - TGAGGTCAAGGAGTTCAAGACCAAGCAGCTGGCCAACATGGTAAACCCCTGTCTACTAAAA - 12720
 12721 - TACAAAAAATTAGCCAGGTGTGGTGTGCACTGGCTGTAGTCCAGCTACTCAGGAGGCTG - 12780
 12781 - AGGCAGGAGAATTGCTTGAACCCAGGAGGAGGAGGTGCAATGAGCAAGATTGTGCTAC - 12840
 12841 - TGCACCTAGCCTGGGTGATATACCGAGACTCCATCTCAAAAAAAAAAAAAAGC - 12900
 12901 - AGGATGTCACTCCCTTGTCACTGCCTGGCTGCCACCCAGGCAGTCATTTGGAT - 12960

Fig. 24 (continued; 6/9)

12961 - CTTCCCTGCCAGTCACCTGGTCTGGCGCTTCTCATGAGAAGGGAGACCTGC - 13020
 13021 - AGCCCCCTTACAGGGCTGGCAGAGGACCTGCTCTGGATTAGGCCCTTCCTAGCCCCTGG - 13080
 13081 - GGTGTGGCAGTGGGTGAGACCGGAAGATCTGCCCTTAGGTTCATAGGCCAAAGTGAT - 13140
 13141 - GATCGTGTGTGCAGGACCTAGAGGGCGCTCCCTGACCCACCCCTTCCCTGCCATACTT - 13200
 13201 - CATCCTCTGGAACAAAGCTGCTTGGTTGAGGGAGTTGGTTGGTTCTTATCCC - 13260
 13261 - TCAGCGCTGAGACATAGAGGCTCCTGGCCACTACAGTGAGACACGAACCTCAAGAAC - 13320
 13321 - TGAATACCCCCGTTTCTCTCCCGCCAAGGCAAAAAGGACTTAGTACTACCTGTGGAG - 13380
 13381 - AAGGAGGTGCAGGACTACCAGGCCCTGCTCTTGCAATTACAGGCCCTCCCCAGACAGAC - 13440
 13441 - ACAGGCACCCCATCACACCCAAACTGGACTTACCTGCTAGGCACCTTCCCTCCCCATC - 13500
 13501 - CAAAAAAATGGAGTTATTTCCCTTATTCAGCAAGTCCAGTTGATTTACCTTGAAAGT - 13560
 13561 - AGCACCTGAGTCCTCACCTCTCCATCCCTCTCACCTGACACAGGTCTGCAG - 13620
 13621 - CGCTCCTCTAGTAGGCAGGACAGCCATTCTGGGATGCACATGTCTAGTCTTGCCTA - 13680
 13681 - GATATGGCAAGTCTTGCCAAGTCTGAGCTAGGCTGTTATGTTCTAGAGGCTTGTGTTTG - 13740
 13741 - CCCATTCTCCATTACAAGAGAACAGGGACACAGAAGTGAGGGCTTCCAGCCCCATA - 13800
 13801 - GGTGATCAATCCTGGGTCAAGAGATTGAGTGTGTTATTGCTTGCCTCTGGGAGCAG - 13860
 13861 - ATTCCATCCATAAACATGTGCTTACCAAGGTCTGACTCACTGGAGAGAACGACGTGA - 13920
 13921 - GGTTGAAAGCTGACCTCCAGAGACTTGGGCCATGTTGTGTTACACATGGGAGTC - 13980
 13981 - CATCATATCAGATTGAGATGGGGCTGGCAAAGTGCCTGGTCTGTGGCTGTGGGCT - 14040

14041 - ACCCTGAGAAAGGGAGCGCCTGACAAGCCACTGCTCCCACCATCTTGTGCAGCATAT - 14100
 - H I

14101 - CGACAAAGTCTTCAAACACAAAGGACCTACAAACAGCAGCTGGTGGATGCCAAGCTCCAGCA - 14160
 - D K V F K H K D L Q Q Q L V D A K L Q Q

14161 - GGCCCAGGAGATGCTAAAGGAGGCAGAAGAGCGGCACCAGCGGGAGAAGGATTTGTGAG - 14220
 - A Q E M L K E A E E R H Q R E K D F

14221 - GCTCAGGCCAGGGTTGGGTGGGGTGTGGAGGAGACAGGCTGGCTCTGGCTCAGC - 14280
 14281 - TCATAGCCGGTTATGGGAGAAGTCTGCCAGACCAGGCACAGATTCCCTGAGTACCA - 14340
 14341 - GTCTGAGAGCAGGAAGCCTCAGTGGGTCTGGCTTGTGGCTAAAACCAACATAGCCC - 14400

14401 - CTGGGGCTTCTGACAGGATCTGGGTTCTGTCTTGGAAATAGCTCCTGAAAGAGGCAGT - 14460
 - L L K E A V

14461 - AGAGTCCCAGAGGATGTGTGAGCTGATGAAGCAGCAAGAGACCCACCTGAAGCAACAGGT - 14520
 - E S Q R M C E L M K Q Q E T H L K Q Q

14521 - GAGAGCATATAACCTGACCCCTGTGCCCTCAAGTTCCCTCACTGGCCCCATCCTGGGG - 14580
 14581 - TAGTGAATGGGACCCCTCATTCTAGGACTGGCTGTGCTCTGGCTGCTATGACGCCCTGGT - 14640
 14641 - TGAGCTTAGGTGGGCTCAGAGGACTTCATTGTAGCTCAGAAATGTATTGCTTTGAGGA - 14700
 14701 - GGTAGGAACAGAAGAGTTGAAATCAACATAAAGGAAAATAAGTCACCCCTAAGTCT - 14760
 14761 - CCTACTTCCAGGCTAGCATTGGATTATATCCTTCAAATATAGCTTGCTTGT - 14820
 14821 - TTTAAGGAAAATAGTATCTCAATAGAATTACTGGTCAGAGAGTCAGGACGGGTCTGAG - 14880
 14881 - TGTGTTGACCAGAGTGCCTCCAGAGAAACCCAGTCTATCTGTGGCTGCTTCTCCCC - 14940

14941 - ACAGCTTGCCTATACACAGAGAAGTTGAGGAGTTCCAGAACACACTTCCAAAAGCAG - 15000
 - L A L Y T E K F E E F Q N T L S K S S

Fig. 24 (continued; 7/9)

15001 - CGAGGTATTCAACCACATTCAAGCAGGAGATGGAAAAGGTAACGTGGTCCAGGCCAGGCA - 15060
 - E V F T T F K Q E M E K

15061 - TGGCTGCTGGGGCATAAGCTGCTTCATTCAAAATTGTTGGGCCTGCCTTCAGGAAGCTCC - 15120
 15121 - CATCTGGGGTGTCTCAAGGGCAGGGCTGTAGGAAGGTTCACAGCCTTCCCCTTGAG - 15180
 15181 - GCAGTATCAGTGGTATGTATACACTCCAGGTTGCCAGGGAAATGGGGCAGTCTTCTG - 15240
 15241 - TTTGTTGGTTTTGGGGGTTGTTGTTGTTGTTGTTGTTGAGA - 15300
 15301 - TGGAGACTCACCTATTGCCAGGCTGGAGTGCAGTGCATGATCTCAGCTCATTCAGCC - 15360
 15361 - TTTGCCCGGGTCAAGTGAATTCTCCTGCCTCAGCCTCCTGACTAGCTGGAATTACAG - 15420
 15421 - GCGCGTGCCACCAGCCTGGCTAATTTTCTTTTTGTATTTTAGTAGAG - 15480
 15481 - ACGGGGTTTCACCAGTGGCCAGGCTGGCTCGAACACTTGGCCTCAAGTGAATGCC - 15540
 15541 - GCCTGGCCTCCAAAGTGTGGATTATAGCGTGAGCCACCATGCCTGGCCCTTACCC - 15600
 15601 - ATTCCCTGTTATTGGTGGTGGACACCTCTGACTTCCTGGTGGTGGACAGAGGGC - 15660
 15661 - ATTGACTGCATCCTGTAATGCCCTGGCCTTGGGATCAATCATCCCCACCTGGAGACA - 15720
 15721 - CAGGTGCAGTCCCCACCTGGAGACACAGACCTGGAGAGGCCAGCTGACCATTCCCT - 15780

15781 - TCTGTCTGTCACATAACCTAGATGACTAAGAAGATCAAGAAGCTGGAGAAAGAAACCACC - 15840
 - M T K K I K K L E K E T T

15841 - ATGTACCGGTCCCAGGGAGAGCAGCAACAAGGCCCTGCTTGAGATGGCTGAGGAGGTGG - 15901
 - M Y R S R W E S S N K A L L E M A E E

15902 - GCTGTCTGTGATCTGCAGCCAGGGTGGGGGTGTGCACTTAGCGCATATCAGGCCCTTCC - 15961
 15962 - TGTATGTTCTACCCATCAGTGCACACAGCTAGCATCAGGTAGAGGTGAGATTGCACACAA - 16021
 16022 - TGTCCAAGTCAAAGTTAATGCTGTTCTCCCCATGGAGGTGGTAGCCAGTGGTAG - 16081
 16082 - GTCTCCAGTGGGAGTGAAGGGAGCAAATGGAAGAAAGGAATAAAAGAGCAGAAAAAAACG - 16141
 16142 - GGTGCCAGTGTGCTGGTTACATGTAAGCAGCCCAGGTAGTTGTGATTTCACAG - 16201
 16202 - CTTGTAATGTAGAAGAAAGGAACAAACGATGGAGCAGCAACTGCAAGCCAGACCTTGCTG - 16261
 16262 - AAAGTTGGGTTTTTGCTTGTGCTGCTGAATGTTTAGGTACGTTGTTCAT - 16321
 16322 - TGAACCTCTCTGAGCTCTGAGGATGGTATTAGTAGCTCTGTTTATAGATGAGACAGG - 16381
 16382 - CTAAAAGTCAAGTCCTTGCAAGGTACGTGGTAGATAATGGAGGAATACGTTATCT - 16441
 16442 - CCAAGCCGTGCCCTTCTGACCATGCTGCCACCTGACAGCCTAGTCATGGCTTCA - 16501
 16502 - ACTAGGACTGTTCTAAAGGGGCCAGCTTGGACTCGGTCTGCTCTAGCCTTGTAA - 16561
 16562 - AGTGTGGCCAGTGGTAGGTAAGTGGAGGTTGATGGGACGGCACTGAAGGT - 16621

16622 - CTCATTTCTTCCTAGAAAACAGTCGGGATAAAGAACTGGAGGGCCTGCAGGTAAAAA - 16681
 - K T V R D K E L E G L Q V K I

16682 - TCCAACGGCTGGAGAAGCTGTGCCGGCACTGCAGACAGAGCGCAATGACCTGAACAAGA - 16741
 - Q R L E K L C R A L Q T E R N D L N K R

16742 - GGGTACAGGACCTGAGTGCTGGTGGCAGGGCTCCCTCACTGACAGTGGCCCTGAGAGGA - 16801
 - V Q D L S A G G Q G S L T D S G P E R R

16802 - GGCCAGAGGGCCTGGGCTCAAGCACCCAGCTCCCCAGGGTACAGAAGCGCCTTGCT - 16861
 - P E G P G A Q A P S S P R V T E A P C Y

16862 - ACCCAGGAGCACCGAGCACAGAACATCAGGCCAGACTGGCCTCAAGAGGCCACCTCCG - 16921
 - P G A P S T E A S G Q T G P Q E P T S A

16922 - CCAGGGCCTAGAGAGCCTGGTGGTCATGCTGGGAAGGGAGCGGCAGGCCAGCCAGG - 16981
 - R A *

Fig. 24 (continued; 8/9)

16982	- CCTGGCCCATAAAAGGCTCCCATGCTGAGCAGCCCATTGCTGAAGCCAGGATGTTCTGAC	- 17041
17042	- CTGGCTGGCATCTGGCACTTGCAATTGGATTTGTGGTCAGTTTACGTACATAGGG	- 17101
17102	- CATTGCAAGGCCTTCAAATGCATTTAACCTGTAAGTGTACAGTGGGCTGCATTGG	- 17161
17162	- GGATGGGGTGTGTACAGATGAAGTCACTGGCTTGTGAGCTGAAGAGTCTTGAGAG	- 17221
17222	- GGGCTGTCATCTGTAGCTGCCATCACAGTGAGTTGGCAGAAGTGACTTGAGCATTCTCT	- 17281
17282	- GTCTGATTGAGGCTCAGACCCCTCCCTGCCCTCAGAGCTCAAGACAAGTAATACACCC	- 17341
17342	- AGGTCTGACTGCATTGTCAGCAGGGCTTGCTGGTCAGCTCAGGCCCTCCTAG	- 17401
17402	- CTGCTCTGGAGGCTCCTTGATCTCTAGACCTGGAAAAGGTGTCCTAGGCAGAGCCCT	- 17461
17462	- GGCAGGGCGCTCAGAGCTGGGATTGCTGCCTGGAAACAAGGGACCTGGAGAATGTTTT	- 17521
17522	- GCGTGGGATGATGTGCTGGTCAGGAGCCCTGGGCATCGCTCCCTGCCCTTGGTAG	- 17581
17582	- TGCCAGGACCAGGCCAATGATGCTTCAGTAGCCTTATCATTACAGGTGCCTCTCTAG	- 17641
17642	- CCTGCACAAATGATTGACAAGAGATCACCCAAAGGATTATTCGAAAGGTGTTTTTCT	- 17701
17702	- TTATTTCTTTCTTTTTTTCTTTCTTTCTTTCTTTGCACATGACAGTGT	- 17761
17762	- TGTATTGAGGACCTTCCAAGGAAGAGGGATGCTGTAGCAGTGGCCTGGGTGCCTGGCC	- 17821
17822	- TCCAGTGTCCCACCTCCTCACCAACCCCCACTTGGCTCTTGCATCTGATGCTGAGGT	- 17881
17882	- TTCCTGTTGGTGGAGATCAGGTGTTGGTAAAGAAAGGAAAGGGCTCTGATGGCT	- 17941
17942	- TTGCCACAAGCTTACCTGTGGGTTCACTGAGAGGCCACCAACAGTCCCATCAGCA	- 18001
18002	- CTGTCATGCAGCAGTTGCTGGTCCCAGTCCAGTGCCTCTTGCTCATGGGTT	- 18061
18062	- TTTCTGCTCCTGCCACCCCCACATGTGCAATCTCAAGATTGTCCTGATTCTATT	- 18121
18122	- TCCTGGCACCTCCCTGCCTGTCTGGGATTCTACTTCTCTGTGTTGAGGCCATAG	- 18181
18182	- CTGTTGCTAACAGGTAAGAAATGAAATTGAACTATTGACTGGGCCCCAGAAATCCATAA	- 18241
18242	- AATGGCTGCAGACAGTTGTTCTGTGCTCTAACCCCCACTCCAGTACATAACTACT	- 18301
18302	- ATGTAAGTGTAGAGCATTCTATATGCTGAATGTTCTGCTGTTGCAAACCTGCCAGGGT	- 18361
18362	- ATTAGCCAGTGTGTTGCCAAGCAGTTCTGGGACAACAGAACAGAATGACTCAGACCAAGATG	- 18421
18422	- GATAGGATGGTTAGGGCTTGCCTCTGCTGTTCTTGAGACTAGTTCATGTCCTG	- 18481
18482	- CAGGTCCCTTCATCTCCATACCTAGCCACTCTTCTAGCCCTAACCTAAATCTCTCAG	- 18541
18542	- ATAAGTTGGTCACAAAGAATGTTAAGTACTGAATCATGTTGACTGAGACCAGAGATGG	- 18601
18602	- CAAATGAATGGCACACCATTCTCCTCTGCCAGGGCAGGTACACTGATCTGCA	- 18661
18662	- TCAGAGTTGCCTGCTATTCTCTGGTGTACCTTCACATCTAGGTGCCCTCAAGCAGCTGT	- 18721
18722	- GTGAGTGTGAGATCTCTGCATCTGGCTGAGATACTGCTGCTGTGAAGTGTTC	- 18781
18782	- CATGACCTTTCTTCCCCTTGAATCCCTGCTGGAGTAGTCCTGCCCTTCTGC	- 18841
18842	- TCCAGTAGGGCCTTCCCTACCCAGCCCTGTGCCAGGCTAGCTGGTACAAGAGCTG	- 18901
18902	- CCAACCTCACAGAGTGTGCTAGGCAGAGAGGTGCAGGGAAAGAGGCAGAGGTATGCAC	- 18961
18962	- CTTCCCCCTTGAAGAGAGGGAAAGGCCACAGTGGCCACATAATTGCCACTCACAC	- 19021
19022	- TTCACTCTTAATGCCCTGTTGGAGGGACTGGAGCTGCTGGATCCCAGTGTGGTGGT	- 19081
19082	- TAGGAGGCCACAGTGTGAGCAGGGCCAGCTGGGTTCCAGGTCAGGAATGTGGGCC	- 19141
19142	- CAGGCAAGGTGCAGCCTTGCTCACAGCTCCATCCATGTCTAGACCTCAGGCCAGTCTG	- 19201
19202	- CAGATGAGGTTCCCTACCTTTCTTCTCTCATTGACCAATCAACCAATCACTACAGC	- 19261
19262	- TGCTCTGCTTCTGCTTCCAAAGTAGGCCAGGTCTGGGCCAGATGCAAGGGGAGGTGCCT	- 19321
19322	- ATCCATGAGTGAAGGCCAGTGTCTCCTCACCTGGGGTCCCACACTGTGACCTCAG	- 19381
19382	- TTTTAGGACCAAGATCTGTGTTGGTTCTAGATTGCTAGCTTCTCCAGGGACAC	- 19441
19442	- AGCAGGTGAAGCTCAAGAGCGCATGGCTCTGCTAATAGTAAATTGTTTCAGGCCCTGT	- 19501
19502	- CCAGCTGAGAGCTTCACTGTCCACCAGATTCTGAGAGGTGTCAAGCAGCACTTTTTTT	- 19561
19562	- ATTTGTTGTTGTTCCATGAGGTTATCGGACCATGGCTGAGCTCAGGCACTTCTGT	- 19621
19622	- AGGAGACTGTTATTCGTAAGATGGTTATTAACCTCTCACCCCATACGGTGGCC	- 19681
19682	- CTGAGGGCTGACCCGGAGGCCAGTGGAGCTGCCCTGGTCAAGGGGGAGGGCCAAGGCC	- 19741
19742	- TGCTGAGCTGATTCTCCAGCTGCTGCCAGCCTTCCGCCTTGACAGCACAGAGGTGG	- 19801
19802	- TCACCCAGGGACAGCCAGGCACCTGCTCTTGCCCTCTGGGGAAAGGGAGCTGCC	- 19861
19862	- TTCTGCTCTGTAACTGCTTCTTATGGCCACGCCGGCCACTCAGACTTGTGTTGAAGC	- 19921
19922	- TGCACGGCAGCTTGTCTCTGGTATTCAACACAGCCAGGGACTGATTTGA	- 19981
19982	- TGTATTTAAACCACATTAAATAAGAGTGTGCTGCCTACTGTTCTCTGACCTG	- 20041
20042	- TGTATTCCTTGTGATCTGATCCATTGAGCTGCCTCATCATCACTGACTGTTC	- 20101
20102	- AGGTCTGCTGCAGAGGCCATGGTGGTCCCTGGTATCTTACATATTCCACAGTGTCTT	- 20161
20162	- TGAGCAGTCGCCACAGCCTCAGGATGCTGCATATTCACTGAGCTGCCAGGGAGCC	- 20221
20222	- CTTGGCAAAGTTGGCAAGACCCCTGCCTCAGAGAGGATCACACACACACAAAAAGTTT	- 20281

Fig. 24 (continued; 9/9)

20282 - CCCTGACCTGGGGCTCACAGGCTAGTGAAGGGAAAGGTACTTTAGCTATAGACAGGT - 20341
20342 - CAATGGTGCAGAGCAGAGAGGAGGCCCTGCCCTTCAGCAAGGTGAGGGGGTATA - 20401
20402 - CCTGGAATGGCCTCTGAACCACAGGGCAGGTAGAAGATGAACGTATTTAGTGATTAAA - 20461
20462 - TGGTACAGCTGGGAAGCAGGTCCATGGGACTGGGAGAGGGGGTAGGGCTGGGCCAGAGT - 20521
20522 - CTGGGTACCAGGTTAAGGAATGTGGGCTAGATCCAGAGGGCAGGGGGGCAACTGAAGGT - 20581
20582 - GTTTCAATAGGAAATTGATAGGCTCCAGCAGTAAGGCAAAGGCATGGAGCCAGGCATAG - 20641
20642 - GCCATTGAGGCCAGGTTAAGAGGGGTGACACTCATCACTGCTATTGGGTCTGAGCT - 20701
20702 - GTGGGTAGGCTCTATAGCCCTGGCCTGCCAAGGAATTCACAGGGCCCTAATTGTA - 20761
20762 - TGCAATTCTTAAGGAGAGCACATTCTCTGTTCAGTTTACACCCCCCATTACCCACCT - 20821
20822 - CAAGCATGGACTCTATATGGGAGACATGCTGCTGGCCTACCCAGCACCTGTT - 20881
20882 - TCTCTGGGTCTGGGTGGTCAGGCACAAGGATGATATGTGCTGAATGCCAGGAAATG - 20941
20942 - GCAGAGACAACCCACCTGCCCTCCAGCCTCACAAATAGATGTGCCCAATGA - 21001
21002 - CTGTGACAGTCCCAGCAGGCCTCTGACCCTCTAGCTGGTCAGTACATGTTCCA - 21061
21062 - TGCTGGCCATGTTATTCTAGTCAGATCCTCTGGAGGGTGTGGGGGGGGTGCAGCCC - 21121
21122 - AACTCTGGAGATTCCAAGCAAAGCAGCTCTGAGAATAATGAGGTTCTGACCCCCCAGT - 21181
21182 - GAAGCAGCTGAGGATGGGAACCAACAGGGGTGCTCCCTCTGTCAGCAGCATTACCACTGTC - 21241
21242 - TACTCTAGCAGCTCCGGTGGGGAGGGAGAGGGGATTCTGTTCTGCCCCAGTCAGGCCCCT - 21301
21302 - GGTATTGAAAAAGTCGGAATTACTCTTACCCCTGTGGAGTGTCTGAGTGTGGAAG - 21361
21362 - TACCCAGGAAGAACCCCTGAGCAGGTGCCCTCAGGAGCAGTGCCATGGCTCCCCACATC - 21421
21422 - AGCCAAGAGGCCAACCCAGGAAGCCACTCCTGCCCGGGATGGGAAGGTGGCTGGG - 21481
21482 - TGGCTGTGCACTGCCCTGGGCCAGCTCACTTGAGCCTGCTGAGCCGCTGGCAAACA - 21541
21542 - TGAGCCTCTCTCCTGTTGATCAGATGCTGTTCTGGGACCTGCGCCAGGAGCCTGCG - 21601
21602 - AGGGCTTAAATAGCTGCCCTATTGATCTGGCTGCAGGCAGCAGCAGTCACACTGGTC - 21661
21662 - AGCCTCCATCAGGTGCTCAGGTTCCCTGAGGACTGGAGTCAGGTGCCAGGGAATCGCGT - 21721
21722 - GGTCTACCTTATGACCTGGTGCCTCCCCACACCTGTCCTAGGCTGGGGGGTGGGGAGG - 21781
21782 - ACTCCTGTCACTTCATCTGGCAGGAAATACAGCCCCCACCACCTACCAGAGAAAATGTC - 21841
21842 - TGGCATTGAGAGAGAGGGTTTGCCCTAAAAGACTGTTGCTTACTTCAGTAGAATG - 21901
21902 - GGGATGACACTGGTATCTCCTTAAGGGTTGTTATGGGATGAAATGTATGTAAAGTGC - 21961
21962 - TCAATAGGGCACTGGACTCACTCCATTGATGGCTGTTGCTGAGTGTCTCTGAT - 22021
22022 - GCTGCTGCTGTTGCTGCTTGTGCTTCTCTGCTTACATTCTCTCTCACTCACTC - 22081
22082 - ACTCTGTCCTCCTCCCCGCCACCCCTTGACAAAGCCACCACCATTTGTA - 22141
22142 - AGGAACGTAGCTCTCTGAAACTGCCGGAAAGGGAAATCTTTAAAATAGACAT - 22201
22202 - CACACAACCAACAGGGTCCCCTAGGTTAGGCAGGGAGGTGAGTCAGTGAGA - 22255